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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING METABOLIC PATHWAY PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated MP nucleic acid molecules, which encode novel MP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MP proteins, mutated MP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MP genes in this organism.

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING METABOLIC  
PATHWAY PROTEINS**

**Related Applications**

- The present application claims priority to prior filed U.S. Provisional Patent
- 5 Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent  
Application Serial No. 60/142101, filed July 2, 1999, U.S. Provisional Patent  
Application Serial No. 60/148613, filed August 12, 1999, and also to U.S. Provisional  
Patent Application Serial No. 60/187970, filed March 9, 2000. The present application  
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- 10 1, 1999, German Patent Application No. 19931415.2, filed July 8, 1999, German Patent  
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10 German Patent Application No. 19941394.0, filed August 31, 1999, German Patent Application No. 19941396.7, filed August 31, 1999, German Patent Application No. 19942076.9, filed September 3, 1999, German Patent Application No. 19942077.7, filed September 3, 1999, German Patent Application No. 19942079.3, filed September 3, 1999, German Patent Application No. 19942086.6, filed September 3, 1999, German  
15 Patent Application No. 19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, German Patent Application No. 19942095.5, filed September 3, 1999, German Patent Application No. 19942124.2, filed September 3, 1999, and German Patent Application No. 19942129.3, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly  
20 incorporated herein by this reference.

### **Background of the Invention**

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and  
25 pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce  
30 and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have

been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

## 5 Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related  
10 bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as metabolic pathway (MP) proteins.

*C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the  
15 degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the MP nucleic acids of the invention, or modification of the sequence of the MP nucleic acid molecules of the  
20 invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The MP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the  
25 presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain  
30 whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium*

*diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms.

- 5 Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The MP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing an enzymatic step involved in the metabolism of certain fine chemicals, including amino acids, vitamins, cofactors, nutraceuticals,

- 10 nucleotides, nucleosides, and trehalose. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and  
15 Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

- This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an  
20 indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nucleotides, and trehalose may have a direct impact on the overall production of one or more of these desired compounds from this organism. For example, optimizing the activity of a lysine biosynthetic pathway protein or decreasing the activity of a lysine degradative pathway  
25 protein may result in an increase in the yield or efficiency of production of lysine from such an engineered organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the production or efficiency of production of a desired fine chemical. For example, a reaction which is in competition for an intermediate necessary for the production of a desired molecule may be eliminated, or a  
30 pathway necessary for the production of a particular intermediate for a desired compound may be optimized. Further, modulations in the biosynthesis or degradation of, for example, an amino acid, a vitamin, or a nucleotide may increase the overall

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ability of the microorganism to rapidly grow and divide, thus increasing the number and/or production capacities of the microorganism in culture and thereby increasing the possible yield of the desired fine chemical.

The nucleic acid and protein molecules of the invention may be utilized to  
5 directly improve the production or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a  
10 biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of  
15 the desired fine chemical may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose through indirect mechanisms. Metabolism of any one compound is necessarily  
20 intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino  
25 acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes  
30 more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

This invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MP), which are capable of, for example, performing an enzymatic step involved in the metabolism of molecules important for the normal functioning of cells, such as amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose. Nucleic acid molecules encoding an MP protein are referred to herein as MP nucleic acid molecules. In a preferred embodiment, the MP protein performs an enzymatic step related to the metabolism of one or more of the following: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....). The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a

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sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform an enzymatic reaction in a amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to catalyze a reaction in a metabolic pathway for an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose, or one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MP protein, or a biologically active portion thereof.

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Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MP protein by culturing the host cell in a suitable medium. The MP protein  
5 can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MP sequence as a  
10 transgene. In another embodiment, an endogenous MP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MP gene. In another embodiment, an endogenous or introduced MP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still  
15 another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being  
20 particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of  
25 one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 1156) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MP protein or a  
30 portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MP protein or portion thereof can catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a

nutraceutical, a nucleotide, a nucleoside, or trehalose. In another preferred embodiment, the isolated MP protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction involved in one or more pathways for the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.

The invention also provides an isolated preparation of an MP protein. In preferred embodiments, the MP protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated MP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of MP proteins also have one or more of the MP bioactivities described herein.

The MP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MP protein alone. In other preferred embodiments, this fusion protein, when introduced into a *C. glutamicum* pathway for the metabolism of an amino acid, vitamin, cofactor, nutraceutical, results in increased yields and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway of a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MP protein activity or MP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MP protein activity can be an agent which stimulates MP protein activity or MP nucleic acid expression.

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Examples of agents which stimulate MP protein activity or MP nucleic acid expression include small molecules, active MP proteins, and nucleic acids encoding MP proteins that have been introduced into the cell. Examples of agents which inhibit MP activity or expression include small molecules, and antisense MP nucleic acid molecules.

5           Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the  
10 introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

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#### **Detailed Description of the Invention**

The present invention provides MP nucleic acid and protein molecules which are involved in the metabolism of certain fine chemicals in *Corynebacterium glutamicum*, including amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and  
20 trehalose. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where modulation of the activity of a lysine biosynthesis protein has a direct impact on the production or efficiency of production of lysine from that  
organism), or may have an indirect impact which nonetheless results in an increase of  
25 yield or efficiency of production of the desired compound (*e.g.*, where modulation of the activity of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a fatty acid from the bacterium, perhaps due to improved growth or an increased supply of necessary co-factors, energy compounds, or precursor molecules). Aspects of the invention are further explicated below.

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### I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include

5 organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty

10 acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids,

15 Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN:

20 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

#### *A. Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are

25 essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH:

30 Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids

have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3<sup>rd</sup> edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E. (1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of  $\alpha$ -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-

step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain  $\beta$ -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3<sup>rd</sup> ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3<sup>rd</sup> ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

### 30 *B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses*

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although

they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B<sub>1</sub>) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B<sub>2</sub>) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B<sub>6</sub>' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic

acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- $\beta$ -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of  $\beta$ -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to  $\beta$ -alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B<sub>5</sub>), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the  $\alpha$ -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B<sub>12</sub>) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B<sub>12</sub> is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B<sub>6</sub>, pantothenate, and

biotin. Only Vitamin B<sub>12</sub> is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

5    C. *Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses*

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic  
10   structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or  
15   their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

20       Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the  
25   development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for  
30   chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and

Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

- 5           The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology,
- 10   Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or
- 15   adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP).
- 20   The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

25   D. Trehalose Metabolism and Uses

- Trehalose consists of two glucose molecules, bound in  $\alpha$ ,  $\alpha$ -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S.
- 30   Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from

many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

## II. Elements and Methods of the Invention

5           The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MP nucleic acid and protein molecules, which play a role in or function in one or more cellular metabolic pathways. In one embodiment, the MP molecules catalyze an enzymatic reaction involving one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic  
10 pathways. In a preferred embodiment, the activity of the MP molecules of the present invention in one or more *C. glutamicum* metabolic pathways for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides or trehalose has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MP molecules of the invention are modulated in activity, such that the  
15 *C. glutamicum* metabolic pathways in which the MP proteins of the invention are involved are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

          The language, "MP protein" or "MP polypeptide" includes proteins which play  
20 a role in, *e.g.*, catalyze an enzymatic reaction, in one or more amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathways. Examples of MP proteins include those encoded by the MP genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "MP gene" or "MP nucleic acid sequence" include nucleic acid sequences encoding an MP protein, which consist of a  
25 coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of  
30 production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes

the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a  
5 "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an  
10 organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall  
15 biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or  
20 more of the biosynthetic or degradative enzymes of the invention for amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a  
25 degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of  
30 the invention may improve the production of other fine chemicals besides the amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, and trehalose. Metabolism of any one compound is necessarily intertwined with other biosynthetic and

degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway.

Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, amino acids serve as the structural units of all proteins, yet may be present intracellularly in levels which are limiting for protein synthesis; therefore, by increasing the efficiency of production or the yields of one or more amino acids within the cell, proteins, such as biosynthetic or degradative proteins, may be more readily synthesized. Likewise, an alteration in a metabolic pathway enzyme such that a particular side reaction becomes more or less favored may result in the over- or under-production of one or more compounds which are utilized as intermediates or substrates for the production of a desired fine chemical.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MP DNAs and the predicted amino acid sequences of the *C. glutamicum* MP proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MP protein or a biologically active portion or fragment thereof of the invention can catalyze an enzymatic reaction in one or more amino acid, vitamin,

cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

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*A. Isolated Nucleic Acid Molecules*

One aspect of the invention pertains to isolated nucleic acid molecules that encode MP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or  
10 amplification of MP-encoding nucleic acid (*e.g.*, MP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides  
15 of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic  
20 acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank  
25 the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

30 A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the

sequence information provided herein. For example, a *C. glutamicum* MP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. ~~The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis.~~ Furthermore, oligonucleotides corresponding to an MP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* MP DNAs of the invention. This DNA comprises sequences encoding MP proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated

sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA00007, RXN00023, RXS00116, or RXC00128). Each of the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA02229 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA02229, RX00351, RXS02970, and RXC02390 are translations of the coding regions of the nucleotide sequences of nucleic acid molecules RXA02229, RX00351, RXS02970, and RXC02390, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:5, designated, as indicated on Table 1, as "F RXA01009", is an F-designated gene, as are SEQ ID NOs: 73, 75, and 77 (designated on Table 1 as "F RXA00007", "F RXA00364", and "F RXA00367", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include *C. glutamicum* those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs

of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MP protein. The nucleotide sequences determined from the cloning of the MP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MP  
5 homologues in other cell types and organisms, as well as MP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one  
10 of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone MP homologues. Probes based on the MP nucleotide sequences can be used to detect transcripts or  
15 genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme cofactor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MP protein, such as by measuring a level of an MP-encoding  
20 nucleic acid in a sample of cells from a subject *e.g.*, detecting MP mRNA levels or determining whether a genomic MP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-  
25 numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or  
30 equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the

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protein or portion thereof is able to catalyze an enzymatic reaction in a *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside or trehalose metabolic pathway. Protein members of such metabolic pathways, as described herein, function to catalyze the biosynthesis or degradation of one or more of: amino acids, vitamins, cofactors, nutraceuticals, nucleotides, nucleosides, or trehalose. Examples of such activities are also described herein. Thus, "the function of an MP protein" contributes to the overall functioning of one or more such metabolic pathway and contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the MP nucleic acid molecules of the invention are preferably biologically active portions of one of the MP proteins. As used herein, the term "biologically active portion of an MP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MP protein that catalyzes an enzymatic reaction in one or more *C. glutamicum* amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathways, or has an activity as set forth in Table 1. To determine whether an MP protein or a biologically active portion thereof can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MP protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the MP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same MP protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00115 (SEQ ID NO:185), a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00131 (SEQ ID NO:991), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00219 (SEQ ID NO:345). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%,

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74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MP nucleotide sequences set forth in the

5 Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MP proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MP gene may exist among individuals within a population due to natural variation. As used herein, the terms

10 "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MP protein, preferably a *C. glutamicum* MP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MP that are the result of natural variation and that do not alter the

15 functional activity of MP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard

20 hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or

25 more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about

30 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to one of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.

A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a  
5 nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MP protein.

10 In addition to naturally-occurring variants of the MP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded MP protein, without altering the functional ability of the MP protein. For example, nucleotide substitutions leading to  
15 amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MP proteins (e.g., an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MP protein, whereas an "essential" amino acid residue is required for MP protein activity.  
20 Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having MP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MP proteins that contain changes in amino acid residues that are not essential  
25 for MP activity. Such MP proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the MP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the  
30 invention and is capable of catalyzing an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic

acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MP protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic

acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MP activity described herein to identify mutants that retain MP activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (e.g., the entire coding region of SEQ ID NO. 1 (RXA02229) comprises nucleotides 1 to 825). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MP disclosed herein (e.g., the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense

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nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MP mRNA. For

5 example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an

10 antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified

15 nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine,

20 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-

25 methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from

30 the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by  
5 conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or  
10 an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

15 In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-*o*-  
20 methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they  
25 have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MP mRNA transcripts to thereby inhibit translation of MP mRNA. A ribozyme having specificity for an MP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MP DNA disclosed herein (*i.e.*, SEQ ID NO: 1  
30 (RXA02229). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MP-encoding mRNA. See, *e.g.*, Cech *et al.*

U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

- 5           Alternatively, MP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MP nucleotide sequence (*e.g.*, an MP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and
- 10   Maher, L.J. (1992) *Bioassays* 14(12):807-15.

#### *B. Recombinant Expression Vectors and Host Cells*

- Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MP protein (or a portion thereof). As
- 15   used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of
- 20   autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to
- 25   which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,
- 30   such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

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The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is

5 operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory

10 sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancers and other expression control elements (*e.g.*, terminators, polyadenylation signals, or other elements of mRNA secondary structure). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).

15 Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI<sup>q</sup>*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *arny*, *SPO2*,  $\lambda$ -*P<sub>R</sub>*- or  $\lambda$ -*P<sub>L</sub>*, which are used preferably in bacteria.

20 Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MF $\alpha$* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or *ubiquitin*- or *phaseolin*-promoters. It is also possible to use artificial promoters. It will be appreciated by one of

25 ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MP proteins, mutant forms of MP proteins, fusion proteins, etc.).

30 The recombinant expression vectors of the invention can be designed for expression of MP proteins in prokaryotic or eukaryotic cells. For example, MP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus

- expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.
- 15            Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically
- 20            serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion
- 25            moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase

30            (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from

the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- 5           Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1,  $\lambda$ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
- 10   Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
- 15   host strains BL21(DE3) or HMS174(DE3) from a resident  $\lambda$  prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
- 20   of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

- One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the
- 25   recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum*
- 30   (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), , 2  $\mu$ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) 5 *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge 10 University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the MP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* 15 (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include 20 those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: 25 New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the 30 expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both

prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

- 5 In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* 10 (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), 15 pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) 20 *Genes Dev.* 3:537-546).

- The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an 25 RNA molecule which is antisense to MP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA.
- 30 The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell

type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant  
5 expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be  
10 identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other  
15 suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms  
20 "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium  
25 chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

30 For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these

integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be  
5 introduced into a host cell on the same vector as that encoding an MP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which  
10 contains at least a portion of an MP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MP gene. Preferably, this MP gene is a *Corynebacterium glutamicum* MP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous  
15 recombination, the endogenous MP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the  
20 endogenous MP protein). In the homologous recombination vector, the altered portion of the MP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MP gene to allow for homologous recombination to occur between the exogenous MP gene carried by the vector and an endogenous MP gene in a microorganism. The additional flanking MP nucleic acid is of sufficient length for successful homologous  
25 recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) *Cell* 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MP gene has homologously recombined with the  
30 endogenous MP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

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For example, inclusion of an MP gene on a vector placing it under control of the lac operon permits expression of the MP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MP gene in a host cell is disrupted (*e.g.*,  
5 by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or  
10 inducer) of an MP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present  
15 invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MP protein. Accordingly, the invention further provides methods for producing MP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of  
20 invention (into which a recombinant expression vector encoding an MP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MP protein) in a suitable medium until MP protein is produced. In another embodiment, the method further comprises isolating MP proteins from the medium or the host cell.

25

### *C. Isolated MP Proteins*

Another aspect of the invention pertains to isolated MP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA  
30 techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MP protein in which the protein is separated from cellular components of the cells in which

it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MP protein having less than about 30% (by dry weight) of non-MP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MP protein, still  
5 more preferably less than about 10% of non-MP protein, and most preferably less than about 5% non-MP protein. When the MP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The  
10 language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MP protein having less than about 30% (by dry weight) of chemical  
15 precursors or non-MP chemicals, more preferably less than about 20% chemical precursors or non-MP chemicals, still more preferably less than about 10% chemical precursors or non-MP chemicals, and most preferably less than about 5% chemical precursors or non-MP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism  
20 from which the MP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MP protein in a microorganism such as *C. glutamicum*.

An isolated MP protein or a portion thereof of the invention can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide,  
25 nucleoside, or trehalose metabolic pathway, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to catalyze an enzymatic  
30 reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MP protein of

the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the MP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MP proteins of the present invention also preferably possess at least one of the MP activities described herein. For example, a preferred MP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can catalyze an enzymatic reaction in an amino acid, vitamin, cofactor, nutraceutical, nucleotide, nucleoside, or trehalose metabolic pathway, or which has one or more of the activities set forth in Table I.

In other embodiments, the MP protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%,

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78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MP activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an MP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MP protein, e.g., an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an MP protein, which include fewer amino acids than a full length MP protein or the full length protein which is homologous to an MP protein, and exhibit at least one activity of an MP protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MP protein include one or more selected domains/motifs or portions thereof having biological activity.

MP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MP protein is expressed in the host cell. The MP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MP protein can be isolated from cells (e.g., endothelial

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cells), for example using an anti-MP antibody, which can be produced by standard techniques utilizing an MP protein or fragment thereof of this invention.

The invention also provides MP chimeric or fusion proteins. As used herein, an MP "chimeric protein" or "fusion protein" comprises an MP polypeptide operatively  
5 linked to a non-MP polypeptide. An "MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to MP, whereas a "non-MP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MP protein, *e.g.*, a protein which is different from the MP protein and which is derived from the same or a different organism. Within the  
10 fusion protein, the term "operatively linked" is intended to indicate that the MP polypeptide and the non-MP polypeptide are fused in-frame to each other. The non-MP polypeptide can be fused to the N-terminus or C-terminus of the MP polypeptide. For example, in one embodiment the fusion protein is a GST-MP fusion protein in which the MP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins  
15 can facilitate the purification of recombinant MP proteins. In another embodiment, the fusion protein is an MP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an MP protein can be increased through use of a heterologous signal sequence.

Preferably, an MP chimeric or fusion protein of the invention is produced by  
20 standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid  
25 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric  
30 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MP-

encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MP protein.

Homologues of the MP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MP protein. As used herein, the term "homologue" refers to a variant form of the MP protein which acts as an agonist or antagonist of the activity of the MP protein. An agonist of the MP protein can retain substantially the same, or a subset, of the biological activities of the MP protein. An antagonist of the MP protein can inhibit one or more of the activities of the naturally occurring form of the MP protein, by, for example, competitively binding to a downstream or upstream member of the MP cascade which includes the MP protein. Thus, the *C. glutamicum* MP protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways in which MP proteins play a role in this microorganism.

In an alternative embodiment, homologues of the MP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MP protein for MP protein agonist or antagonist activity. In one embodiment, a variegated library of MP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MP sequences therein. There are a variety of methods which can be used to produce libraries of potential MP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the MP protein coding can be used to generate a variegated population of MP fragments for screening and subsequent selection of homologues of an MP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MP coding sequence with a nuclease under conditions wherein nicking occurs only  
5 about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression  
10 vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for  
15 rapid screening of the gene libraries generated by the combinatorial mutagenesis of MP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a  
20 desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

25 In another embodiment, cell based assays can be exploited to analyze a variegated MP library, using methods well known in the art.

#### *D. Uses and Methods of the Invention*

The nucleic acid molecules, proteins, protein homologues, fusion proteins,  
30 primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C.*

*glutamicum* sequences of interest; evolutionary studies; determination of MP protein regions required for function; modulation of an MP protein activity; modulation of the activity of an MP pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

- 5           The MP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the
- 10   extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is not pathogenic to humans, it is related to species which are human pathogens, such as *Corynebacterium diphtheriae*.
- 15   *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the
- 20   inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at
- 25   least 5,000 deaths since 1990.

- In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in
- 30   the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum*

are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to  
5 identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable  
10 labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that  
15 these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells;  
20 by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the  
25 enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MP nucleic acid molecules of the invention may result in the production of MP proteins having functional differences from the wild-type MP  
30 proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention also provides methods for screening molecules which modulate the activity of an MP protein, either by interacting with the protein itself or a substrate or binding partner of the MP protein, or by modulating the transcription or translation of an MP nucleic acid molecule of the invention. In such methods, a microorganism  
5 expressing one or more MP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MP protein is assessed.

When the desired fine chemical to be isolated from large-scale fermentative culture of *C. glutamicum* is an amino acid, a vitamin, a cofactor, a nutraceutical, a  
10 nucleotide, a nucleoside, or trehalose, modulation of the activity or efficiency of activity of one or more of the proteins of the invention by recombinant genetic mechanisms may directly impact the production of one of these fine chemicals. For example, in the case of an enzyme in a biosynthetic pathway for a desired amino acid, improvement in efficiency or activity of the enzyme (including the presence of multiple copies of the  
15 gene) should lead to an increased production or efficiency of production of that desired amino acid. In the case of an enzyme in a biosynthetic pathway for an amino acid whose synthesis is in competition with the synthesis of a desired amino acid, any decrease in the efficiency or activity of this enzyme (including deletion of the gene) should result in an increase in production or efficiency of production of the desired amino acid, due to  
20 decreased competition for intermediate compounds and/or energy. In the case of an enzyme in a degradation pathway for a desired amino acid, any decrease in efficiency or activity of the enzyme should result in a greater yield or efficiency of production of the desired product due to a decrease in its degradation. Lastly, mutagenesis of an enzyme involved in the biosynthesis of a desired amino acid such that this enzyme is no longer is  
25 capable of feedback inhibition should result in increased yields or efficiency of production of the desired amino acid. The same should apply to the biosynthetic and degradative enzymes of the invention involved in the metabolism of vitamins, cofactors, nutraceuticals, nucleotides, nucleosides and trehalose.

Similarly, when the desired fine chemical is not one of the aforementioned  
30 compounds, the modulation of activity of one of the proteins of the invention may still impact the yield and/or efficiency of production of the compound from large-scale culture of *C. glutamicum*. The metabolic pathways of any organism are closely

interconnected; the intermediate used by one pathway is often supplied by a different pathway. Enzyme expression and function may be regulated based on the cellular levels of a compound from a different metabolic process, and the cellular levels of molecules necessary for basic growth, such as amino acids and nucleotides, may critically affect the viability of the microorganism in large-scale culture. Thus, modulation of an amino acid biosynthesis enzyme, for example, such that it is no longer responsive to feedback inhibition or such that it is improved in efficiency or turnover may result in increased cellular levels of one or more amino acids. In turn, this increased pool of amino acids provides not only an increased supply of molecules necessary for protein synthesis, but also of molecules which are utilized as intermediates and precursors in a number of other biosynthetic pathways. If a particular amino acid had been limiting in the cell, its increased production might increase the ability of the cell to perform numerous other metabolic reactions, as well as enabling the cell to more efficiently produce proteins of all kinds, possibly increasing the overall growth rate or survival ability of the cell in large scale culture. Increased viability improves the number of cells capable of producing the desired fine chemical in fermentative culture, thereby increasing the yield of this compound. Similar processes are possible by the modulation of activity of a degradative enzyme of the invention such that the enzyme no longer catalyzes, or catalyzes less efficiently, the degradation of a cellular compound which is important for the biosynthesis of a desired compound, or which will enable the cell to grow and reproduce more efficiently in large-scale culture. It should be emphasized that optimizing the degradative activity or decreasing the biosynthetic activity of certain molecules of the invention may also have a beneficial effect on the production of certain fine chemicals from *C. glutamicum*. For example, by decreasing the efficiency of activity of a biosynthetic enzyme in a pathway which competes with the biosynthetic pathway of a desired compound for one or more intermediates, more of those intermediates should be available for conversion to the desired product. A similar situation may call for the improvement of degradative ability or efficiency of one or more proteins of the invention.

This aforementioned list of mutagenesis strategies for MP proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By

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these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any

5 natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not

10 be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: Included Genes

## Lysine biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXA02229	GR00613	2793	3617	DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7)
3	4	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
5	6	F RXA01009				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
7	8	RXC02390	GR00217	4714	5943	MEMBRANE SPANNING PROTEIN INVOLVED IN LYSINE METABOLISM
9	10	RXC01796				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN LYSINE METABOLISM
11	12	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
13	14	RXC00657				TRANSCRIPTIONAL REGULATOR INVOLVED IN LYSINE METABOLISM
15	16	RXC00552				CYTOSOLIC PROTEIN INVOLVED IN LYSINE METABOLISM

## Trehalose

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
17	18	RXN00351	VW0131	37078	38532	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
19	20	F RXA00351	GR00056	1486	2931	ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 56 KD SUBUNIT (EC 2.4.1.15)
21	22	RXA00873	GR00211	3	758	trehalose synthase (EC 2.4.1.-)
23	24	RXA00891	GR00213	1005	4	trehalose synthase (EC 2.4.1.-)

## Lysine biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
25	26	RXA00534	GR00137	4758	3496	ASPARTOKINASE ALPHA AND BETA SUBUNITS (EC 2.7.2.4)
27	28	RXA00533	GR00137	3469	2438	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.11)
29	30	RXA02843	GR00642	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
31	32	RXA02022	GR00613	2063	3169	SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18)
33	34	RXA00044	GR00107	3458	4393	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
35	36	RXA00863	GR00136	896	1639	DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26)
37	38	RXA00864	GR00136	1694	2443	probable 2,3-dihydrodipicolinate N-C6-lyase (cyclizing) (EC 4.3.3.-) - Corynebacterium glutamicum
39	40	RXA02843	GR00642	543	4	2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (EC 2.3.1.117)
41	42	RXN00355	VW0135	31980	30961	MESO-DIAMINOPIMELATE D-DEHYDROGENASE
43	44	F RXA00352	GR00068	861	4	MESO-DIAMINOPIMELATE D-DEHYDROGENASE (EC 1.4.1.16)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
45	46	RXA00972	GR00274	3	1379	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
47	48	RXA02653	GR00752	5237	7234	DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20)
49	50	RXA01393	GR00408	4249	3380	LYSINE EXPORT REGULATOR PROTEIN
51	52	RXA00241	GR00036	5443	6945	L-LYSINE TRANSPORT PROTEIN
53	54	RXA01394	GR00408	4320	5018	LYSINE EXPORTER PROTEIN
55	56	RXA00865	GR00236	2647	3549	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52)
57	58	RXS02021				2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTTRANSFERASE (EC 2.3.1.117)
59	60	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
61	62	RXC00733				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
63	64	RXC00861				PROTEIN INVOLVED IN LYSINE METABOLISM
65	66	RXC00866				ZN-DEPENDENT HYDROLASE INVOLVED IN LYSINE METABOLISM
67	68	RXC02095				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN LYSINE METABOLISM
69	70	RXC03185				PROTEIN INVOLVED IN LYSINE METABOLISM

## Glutamate and glutamine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
71	72	RXN00367	VV0196	9744	14273	GLUTAMATE SYNTHASE [NADH] PRECURSOR (EC 1.4.1.14)
73	74	F RXA00007	GR00001	7107	8912	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
75	76	F RXA00364	GR00074	1296	4	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
77	78	F RXA00367	GR00075	1806	964	GLUTAMATE SYNTHASE (NADPH) LARGE CHAIN PRECURSOR (EC 1.4.1.13)
79	80	RXN00076	VV0154	2752	4122	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
81	82	F RXA00075	GR00012	2757	3419	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
83	84	RXN00198	VV0181	7916	7368	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
85	86	F RXA00198	GR00031	2	283	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
87	88	RXN00365	VV0196	14607	15233	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
89	90	F RXA00365	GR00075	630	4	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
91	92	RXA00366	GR00075	961	605	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
93	94	RXA02072	GR00628	1259	2599	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
95	96	RXA00323	GR00057	3855	5192	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
97	98	RXA00335	GR00057	19180	17750	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
99	100	RXA00324	GR00057	5262	8396	GLUTAMATE SYNTHASE (NADPH) SMALL CHAIN (EC 1.4.1.13)
101	102	RXN03176	VV0332	2	862	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4)
103	104	F RXA02879	GR10017	2	862	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
105	106	RXA00278	GR00043	2612	1581	GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE (EC 2.7.7.42)
107	108	RXA00727	GR00193	614	1525	GLUTAMINE SYNTHETASE (EC 6.3.1.2)
						GLUTAMINASE (EC 3.5.1.2)
						GLUTAMINASE (EC 3.5.1.2)
						GLUTAMINE-BINDING PROTEIN PRECURSOR
						GLUTAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

## Alanine and Aspartate and Asparagine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
109	110	RXA02139	GR00639	6739	4901	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4)
111	112	RXN00116	VV0100	26974	25814	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
113	114	F RXA00116	GR00018	510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
115	116	RXN00618	VV0135	10288	9182	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
117	118	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
119	120	F RXA00627	GR00154	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
121	122	RXA02550	GR00729	1585	275	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
123	124	RXA02193	GR00645	1942	365	ASPARTATE AMONIA-LYASE (EC 4.3.1.1)
125	126	RXA02432	GR00708	2669	1695	L-ASPARAGINASE (EC 3.5.1.1)
127	128	RXN03003	VV0138	680	6	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
129	130	RXN00508	VV0086	4701	5783	ALANINE RACEMASE (EC 5.1.1.1)
131	132	RXN00636	VV0135	20972	19944	ALANINE RACEMASE, BIOSYNTHETIC (EC 5.1.1.1)

## beta-Alanine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
133	134	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
135	136	RXS00870				METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
137	138	RXS02299				ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)

## Glycine and serine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
139	140	RXA01561	GR00435	1113	2042	L-SERINE DEHYDRATASE (EC 4.2.1.13)
141	142	RXA01850	GR00525	481	1827	L-SERINE DEHYDRATASE (EC 4.2.1.13)
143	144	RXA00580	GR00156	7343	6042	SERINE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
145	146	RXA01821	GR00515	10253	9876	SARCOSINE OXIDASE (EC 1.5.3.1)
147	148	RXN02263	VV0202	11783	12160	SARCOSINE OXIDASE (EC 1.5.3.1)
149	150	F RXA02263	GR00654	33454	33813	SARCOSINE OXIDASE (EC 1.5.3.1)
151	152	RXA02176	GR00641	11454	12581	PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52)
153	154	RXN02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
155	156	F RXA02479	GR00717	393	4	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
157	158	F RXA02758	GR00766	5082	4648	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
159	160	F RXA02759	GR00766	5330	5220	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
161	162	RXA02501	GR00720	15041	13977	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)
163	164	RXN03105	VV0074	15857	15423	SARCOSINE OXIDASE (EC 1.5.3.1)
165	166	RXS01130				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
167	168	RXS03112				D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)

Table 1 (continued)

## Threonine metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
169	170	RXNC0969	VV0149	12053	13387	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
171	172	F RXA00974	GR00274	2623	3015	HOMOSERINE DEHYDROGENASE (EC 1.1.1.3)
173	174	RXA00970	GR00273	161	1087	HOMOSERINE KINASE (EC 2.7.1.39)
175	176	RXA00330	GR00057	12968	14410	THREONINE SYNTHASE (EC 4.2.99.2)
177	178	RXN00403	VV0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
179	180	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
181	182	RXC01207				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF LYSINE AND THREONINE
183	184	RXC00152				MEMBRANE ASSOCIATED PROTEIN INVOLVED IN THREONINE METABOLISM

## Metabolism of methionine and S-adenosyl methionine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
185	186	RXA00115	GR00017	5359	4313	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.31)
187	188	RXN00403	VV0086	70041	68911	HOMOSERINE O-ACETYLTRANSFERASE
189	190	F RXA00403	GR00088	723	1832	HOMOSERINE O-ACETYLTRANSFERASE (EC 2.3.1.11)
191	192	RXS03158				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
193	194	F RXA00254	GR00038	2404	1811	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
195	196	RXA02532	GR00726	3085	2039	CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
197	198	RXS03159				CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9)
199	200	F RXA02768	GR00770	1919	2521	5-methyltetrahydrofolate-homocysteine methyltransferase (methionine synthetase)
201	202	RXA00216	GR00032	16286	15297	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
203	204	RXN00402	VV0086	70787	70188	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
205	206	F RXA00402	GR00088	1	576	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
207	208	RXA00405	GR00089	3289	3801	O-ACETYLHOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
209	210	RXA02197	GR00645	4552	4025	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
211	212	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
213	214	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
215	216	RXN03074	VV0042	2238	1741	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.1.13)
217	218	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.1.13)
219	220	RXN00132	VV0124	3612	5045	ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.1.13)
221	222	F RXA00132	GR00020	7728	7624	ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.1.13)

Table 1 (continued)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
223	224	F RXA01371	GR00398	2339	3634	ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1)
225	226	RXN02085				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
227	228	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
229	230	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
231	232	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
233	234	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
235	236	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
237	238	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
239	240	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDIMES AND ADENOSYLHOMOCYSTEINE

### S-adenosyl methionine (SAM) Biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
241	242	RXA02240	GR00654	7160	8380	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

### Cysteine metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
243	244	RXA00780	GR00206	1689	2234	SERINE ACETYLTRANSFERASE (EC 2.3.1.30)
245	246	RXA00779	GR00206	550	1482	CYSTEINE SYNTHASE (EC 4.2.99.8)
247	248	RXN00402	VV0086	70787	70188	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYL SERINE SULFHYDRYLASE (EC 4.2.99.8)
249	250	F RXA00402	GR00088	1	576	O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
251	252	RXS00405				O-ACETYLMOMOSERINE SULFHYDRYLASE (EC 4.2.99.10) / O-ACETYLSERINE SULFHYDRYLASE (EC 4.2.99.8)
253	254	RXC00164				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM
255	256	RXC01191				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN CYSTEINE METABOLISM

Table 1 (continued)

## Valine, leucine and isoleucine

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
257	258	RXAC2646	GR00751	3856	2588	THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16)
259	260	RXA00766	GR00204	5091	4249	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
261	262	RXN01690	VV0246	1296	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
263	264	F RXA01690	GR00473	1248	196	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
265	266	RXN01026	VV0143	9171	7513	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
267	268	F RXA01026	GR00294	1	1602	3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (EC 4.2.1.33)
269	270	RXNC1127	VV0157	4491	3472	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
271	272	F RXA01132	GR00315	1349	1651	3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85)
273	274	RXNC0536	VV0219	6128	7498	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
275	276	F RXA00536	GR00137	6128	7360	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.1)
277	278	RXN02965	VV0143	7711	7121	3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
279	280	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE DEHYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
281	282	F RXA01929	GR00555	2766	1960	/ DECARBOXYLASE (EC 4.1.1.44)
283	284	RXN01420	VV0122	15584	14643	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
285	286	RXS01145				4'-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.3.3.2)
287	288	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)

## Arginine and proline metabolism

## Enzymes of proline biosynthesis:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
289	290	RXA02375	GR00689	1449	223	GLUTAMATE 5-KINASE (EC 2.7.2.11)
291	292	RXN02382	VV0213	5162	3867	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
293	294	F RXA02378	GR00690	624	16	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
295	296	F RXA02382	GR00691	2493	1894	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
297	298	RXA02499	GR00720	11883	12692	PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2)
299	300	RXS02157				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
301	302	RXS02262				ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
303	304	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
305	306	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

Table 1 (continued)

## Enzymes of proline degradation:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
307	308	RXN00023	VW0127	68158	64703	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
309	310	F RXA00023	GR00003	2	454	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
311	312	F RXA02284	GR00660	3028	5	PROLINE DEHYDROGENASE (EC 1.5.99.8) / DELTA-1- PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.1.12)
313	314	RXC02498				PROTEIN INVOLVED IN PROLINE METABOLISM

## Synthesis of 3-Hydroxy-proline:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig
315	316	RXA01491	GR00423

## Enzymes of ornithine, arginine and spermidine metabolism:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
317	318	RXA02155	GR00640	1913	3076	GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) / AMINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1)
319	320	RXA02156	GR00640	3125	4075	ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
321	322	RXN02153	VW0122	14106	13327	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
323	324	F RXA02153	GR00640	757	1536	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
325	326	RXA02154	GR00640	1536	1826	N-ACETYLGLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE
327	328	RXA02157	GR00640	4079	5251	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
329	330	RXS02970				ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
331	332	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
333	334	RXA02158	GR00640	5268	6224	ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3)
335	336	RXA02160	GR00640	6914	8116	ARGINOSUCCINATE SYNTHASE (EC 6.3.4.5)
337	338	RXN02162	VW0122	6883	5253	ARGINOSUCCINATE LYASE (EC 4.3.2.1)
339	340	F RXA02161	GR00640	8180	8962	ARGINOSUCCINATE LYASE (EC 4.3.2.1)
341	342	F RXA02162	GR00640	8949	9611	ARGINOSUCCINATE LYASE (EC 4.3.2.1)
343	344	RXA02262	GR00654	32291	33436	ORNITHINE CYCLODEAMINASE (EC 4.3.1.12)
345	346	RXA00032	GR00032	19289	20230	SPERMIDINE SYNTHASE (EC 2.5.1.16)
347	348	RXA01508	GR00424	12652	14190	SPERMIDINE SYNTHASE (EC 2.5.1.16)
349	350	RXA01757	GR00498	2942	2142	PUTRESCINE OXIDASE (EC 1.4.3.10)
351	352	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
353	354	RXN02154	VW0122	13327	13037	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.1.38)
355	356	RXS00147				CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
357	358	RXS00905				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
359	360	RXS00906				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
361	362	RXS00907				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
363	364	RXS02001				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
365	366	RXS02101				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
367	368	RXS02234				CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
369	370	F RXA02234	GR00654	1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
371	372	RXS02565				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
373	374	RXS02937				N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)

  

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
375	376	RXA02194	GR00645	2897	2055	ATP PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.17)
377	378	RXA02195	GR00645	3186	2917	PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE (EC 3.6.1.31)
379	380	RXA01057	GR00306	4726	4373	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19)
381	382	RXA01100	GR00306	7072	6335	PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE (EC 5.3.1.16)
383	384	RXA01101	GR00306	7726	7094	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
385	386	RXNC1657	VW00110	39950	39351	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
387	388	F RXA01657	GR00460	2444	2944	AMIDOTRANSFERASE HISH (EC 2.4.2.-)
389	390	RXAC1098	GR00306	5499	4726	HISF PROTEIN
391	392	RXNC1104	VW0059	7037	6432	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19)
393	394	F RXA01104	GR00306	10927	10322	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (EC 4.2.1.19) / HISTIDINOL-PHOSPHATASE (EC 3.1.3.15)
395	396	RXNC0446	VW0112	24181	23318	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
397	398	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
399	400	RXAC1105	GR00306	12044	10947	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
401	402	RXA01106	GR00306	13378	12053	HISTIDINOL DEHYDROGENASE (EC 1.1.1.23)
403	404	RXC00930				PROTEIN INVOLVED IN HISTIDINE METABOLISM
405	406	RXC01096				PROTEIN INVOLVED IN HISTIDINE METABOLISM
407	408	RXC01656				PROTEIN INVOLVED IN HISTIDINE METABOLISM
409	410	RXC01158				MEMBRANE SPANNING PROTEIN INVOLVED IN HISTIDINE METABOLISM

## Histidine metabolism

## Metabolism of aromatic amino acids

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
411	412	RXA02458	GR00712	3056	4345	3-PHOSPHOSHIMIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
413	414	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.)
415	416	RXN00954	VW0247	3197	2577	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
417	418	F RXA00954	GR00263	3	590	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
419	420	RXN00957	VW0208	1211	2764	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)
421	422	F RXA00957	GR00264	3	1130	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	Table 1 (continued)		
				NT Start	NT Stop	Function
423	424	RXA02687	GR00754	11306	12250	CHORISMATE MUTASE (EC 5.4.99.5) / PREPHENATE DEHYDRATASE (EC 4.2.1.51)
425	426	RXN01698	VW0134	11507	12736	CHORISMATE SYNTHASE (EC 4.6.1.4)
427	428	F RXA01698	GR00477	2	991	CHORISMATE SYNTHASE (EC 4.6.1.4)
429	430	RXA01095	GR00306	3603	2821	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48)
431	432	RXA00955	GR00263	586	2007	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (EC 4.1.1.48) / N-(5'-PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24)
433	434	RXA02814	GR00795	598	128	ISOCHORISMATE MUTASE
435	436	RXA00229	GR00033	1715	936	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
437	438	RXA02093	GR00629	12444	13247	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
439	440	RXA02791	GR00777	6968	7795	SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25)
441	442	RXA01699	GR00477	984	1553	SHIKIMATE KINASE (EC 2.7.1.71)
443	444	RXA00952	GR00262	97	936	TRYPTOPHAN SYNTHASE ALPHA CHAIN (EC 4.2.1.20)
445	446	RXN00956	VW0247	1140	4	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
447	448	F RXA00956	GR00263	2027	3157	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
449	450	RXA00064	GR00010	2499	3776	TYROSINE AMINOTRANSFERASE (EC 2.6.1.5)
451	452	RXN00448	VW0112	33959	32940	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
453	454	F RXA00448	GR00109	3	668	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
455	456	F RXA00452	GR00110	854	1099	PREPHENATE DEHYDROGENASE (EC 1.3.1.12)
457	458	RXA00584	GR00156	11384	10260	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
459	460	RXA00579	GR00156	5946	4087	PARA-AMINO BENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
461	462	RXA00958	GR00264	1130	1753	PARA-AMINO BENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
463	464	RXN03007	VW0208	3410	3778	ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
465	466	RXN02918	VW0086	25447	25887	TRYPTOPHAN SYNTHASE BETA CHAIN (EC 4.2.1.20)
467	468	RXN01116	VW0182	7497	6886	3-OXOADIPATE COA-TRANSFERASE SUBUNIT B (EC 2.8.3.6)
469	470	RXN01115	VW0182	10347	11099	3-OXOADIPATE ENOL-LACTONE HYDROLASE (EC 3.1.1.24) / 4-CARBOXYMUCONOLACTONE
471	472	RXS00116		510	4	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
473	474	F RXA00116	GR00018			ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
475	476	RXS00391				O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
477	478	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
479	480	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
481	482	RXS00446				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
483	484	F RXA00446	GR00108	4	525	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
485	486	RXS00618				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
487	488	F RXA00618	GR00163	213	746	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
489	490	F RXA00627	GR00164	854	1138	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
491	492	RXS01105				HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.1)
493	494	RXS02315				2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE / 2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
495	496	RXS02550				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
497	498	RXS02319				NAPHTHOATE SYNTHASE (EC 4.1.3.36)
499	500	RXS02908				O-SUCCINYL BENZOIC ACID--COA LIGASE (EC 6.2.1.26)
501	502	RXS03003				ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)
503	504	RXS03026				3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)

Table 1 (continued)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
505	506	RXS03074				S-ADENOSYLMETHIONINE 2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
507	508	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN
509	510	RXC02080				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
511	512	RXC02789				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS
513	514	RXC02295				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS

### Aminobutyrate metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
515	516	RXN03063	VV0035	666	1697	4-aminobutyrate aminotransferase (EC 2.6.1.19)
517	518	RXNC2970	VV0021	4714	5081	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)
519	520	F RXA01009	GR00287	4714	5943	ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11)

### Vitamins, vitamin-like substances (cofactors), nutraceuticals

#### Thiamine metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
521	522	RXA01551	GR00431	2945	4819	THIAMIN BIOSYNTHESIS PROTEIN THIC
523	524	RXA01019	GR00291	6	995	THIAMIN-MONOPHOSPHATE KINASE (EC 2.7.4.16)
525	526	RXA01352	GR00393	609	4	THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (EC 2.5.1.3)
527	528	RXA01381	GR00403	3206	2286	THIF PROTEIN
529	530	RXA01360	GR00394	162	4	THIG PROTEIN
531	532	RXA01361	GR00394	983	378	THIG PROTEIN
533	534	RXA01208	GR00348	229	1032	HYDROXYETHYLTHIAZOLE KINASE (EC 2.7.1.50)
535	536	RXA00838	GR00227	1532	633	APBA PROTEIN
537	538	RXA02400	GR00699	1988	2557	THIAMIN BIOSYNTHESIS PROTEIN X
539	540	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
541	542	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
543	544	RXN01413	VV0050	27306	27905	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
545	546	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
547	548	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
549	550	RXS01807				PYRIDOXINE KINASE (EC 2.7.1.35)
551	552	RXC01021				CYTOSOLIC KINASE INVOLVED IN METABOLISM OF SUGARS AND THIAMIN

Table 1 (continued)

## Riboflavin metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
553	554	RXN02246	VV0130	4388	5371	diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
555	556	F RXA02246	GR00654	14299	15282	RIBG PROTEIN riboflavin-specific deaminase [EC 3.5.4.-]
557	558	RXN02247	GR00654	15286	15918	RIBOFLAVIN SYNTHASE ALPHA CHAIN (EC 2.5.1.9)
559	560	RXN02248	VV0130	6021	7286	GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE
561	562	F RXA02248	GR00654	15932	17197	RIBA PROTEIN - GTP cyclohydrolase II [EC 3.5.4.25]
563	564	RXN02249	VV0130	7301	7777	6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE (EC 2.5.1.9)
565	566	F RXA02249	GR00654	17212	17688	RIBH PROTEIN - 6,7-dimethyl-8-ribityllumazine synthase (dmrl synthase, lumazine synthase, riboflavin synthase beta chain) [EC 2.5.1.9]
567	568	RXA02250	GR00654	17778	18356	RIBX PROTEIN
569	570	RXA01489	GR00423	3410	2388	RIBOFLAVIN KINASE (EC 2.7.1.26) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
571	572	RXA02135	GR00639	2809	1736	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE
573	574	RXA01489	GR00423	3410	2388	PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
575	576	RXN01712	VV0191	8993	8298	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
577	578	F RXA01712	GR00484	2652	2152	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
579	580	RXN02384	VV0213	1386	679	ALPHA-RIBAZOLE-5'-PHOSPHATE PHOSPHATASE (EC 3.1.3.-)
581	582	RXN01560	VV0319	767	438	RIBOFLAVIN-SPECIFIC DEAMINASE (EC 3.5.4.-)
583	584	RXN00667	VV0109	1363	350	DRAP DEAMINASE
585	586	RXC01711				MEMBRANE SPANNING PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
587	588	RXC02380				PROTEIN INVOLVED IN RIBOFLAVIN METABOLISM
589	590	F RXA02380	GR00691	709	56	Predicted nucleotidyltransferases
591	592	RXC02921				CYTOSOLIC PROTEIN INVOLVED IN METABOLISM OF RIBOFLAVIN AND LIPIDS
593	594	RXC01434				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF AROMATIC AMINO ACIDS AND RIBOFLAVIN

## Vitamin B6 metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
595	596	RXA01807	GR00509	7868	7077	PYRIDOXINE KINASE (EC 2.7.1.35), pyridoxal/pyridoxine/pyridoxamine kinase

**Table 1 (continued)**  
**Nicotinate (nicotinic acid), nicotinamide, NAD and NADP**

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
597	598	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
599	600	F RXA02405	GR00701	774	4	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
601	602	F RXA02754	GR00766	3	488	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)
603	604	RXA02112	GR00632	5600	6436	NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLATING) (EC 2.4.2.19)
605	606	RXA02111	GR00632	4310	5593	QUINOLINATE SYNTHETASE A

### NAD Biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
607	608	RXA01073	GR00300	1274	2104	NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1)
609	610	RXN02754	VV0084	22564	23901	NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11)

### Pantothenate and Coenzyme A (CoA) biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
611	612	RXA02299	GR00662	10452	10859	ASPARTATE 1-DECARBOXYLASE PRECURSOR (EC 4.1.1.11)
613	614	RXA01928	GR00555	1957	1121	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
615	616	RXN01929	VV0127	47590	48402	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11) / DECARBOXYLASE (EC 4.1.1.44)
617	618	F RXA01929	GR00555	2766	1960	3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11)
619	620	RXA01521	GR00424	25167	25964	PANTOATE--BETA-ALANINE LIGASE (EC 6.3.2.1)
621	622	RXS01145				KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
623	624	F RXA01145	GR00321	1075	1530	KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
625	626	RXA02239	GR00654	5784	7049	DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN
627	628	RXA00581	GR00156	7572	8540	PANTOTHENATE KINASE (EC 2.7.1.33)
629	630	RXS00838				2-DEHYDROPANTOATE 2-REDUCTASE (EC 1.1.1.169)
631	632	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE

### Biotin metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
633	634	RXN03058	VV0028	8272	8754	BIOTIN SYNTHESIS PROTEIN BIOC

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
635	636	F RXA02903	GR10040	11532	12014	BIOTIN SYNTHESIS PROTEIN BIOC
637	638	RXA00166	GR00025	3650	4309	BIOTIN SYNTHESIS PROTEIN BIOC
639	640	RXA00633	GR00166	3556	2288	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (EC 2.6.1.62)
641	642	RXA00632	GR00166	2281	1610	DETHIOBIOTIN SYNTHETASE (EC 6.3.3.3)
643	644	RXA00295	GR00047	3407	4408	BIOTIN SYNTHASE (EC 2.8.1.6)
645	646	RXA00223	GR00032	23967	22879	NIFS PROTEIN
647	648	RXN00262	VV0123	16681	15608	NIFS PROTEIN
649	650	F RXA00262	GR00040	79	897	NIFS PROTEIN
651	652	RXN00435	VV0112	10037	11209	NIFS PROTEIN
653	654	F RXA00435	GR00100	3563	2949	NIFS PROTEIN
655	656	F RXA02801	GR00782	438	4	NIFS PROTEIN
657	658	RXA02516	GR00723	1724	2986	NIFS PROTEIN
659	660	RXA02517	GR00723	2989	3435	NIFU PROTEIN

## Lipoic Acid

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
661	662	RXA01747	GR00495	2506	3549	LPOIC ACID SYNTHETASE
663	664	RXA01746	GR00495	1614	2366	LPOATE-PROTEIN LIGASE B (EC 6.---)
665	666	RXA02106	GR00632	472	1527	LPOATE-PROTEIN LIGASE A (EC 6.---)
667	668	RXS01183				DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2- OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
669	670	RXS01260				LPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
671	672	RXS01261				LPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

## Folate biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
673	674	RXA02717	GR00758	18281	17400	5,10-METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.7.99.5)
675	676	RXN02027	VV0296	503	1003	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
677	678	F RXA02027	GR00616	500	6	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2)
679	680	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
681	682	RXN01321	VV0082	8868	9788	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
683	684	F RXA01321	GR00384	23	559	FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
685	686	RXA00461	GR00116	428	1279	METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHYLTETRAHYDROFOLATE DEHYDROGENASE (EC 3.5.4.9)
687	688	RXA01514	GR00424	20922	21509	GTP CYCLOHYDROLASE I (EC 3.5.4.16)
689	690	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
691	692	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
693	694	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
695	696	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
697	698	RXA00989	GR00280	2903	1371	FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17)
699	700	RXA01517	GR00424	22752	23228	2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE PYROPHOSPHOKINASE (EC 2.7.6.3)
701	702	RXA00579	GR00156	5946	4087	PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-)
703	704	RXA00958	GR00264	1130	1753	PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (EC 4.1.3.-) / ANTHRANILATE SYNTHASE COMPONENT II (EC 4.1.3.27)
705	706	RXA02790	GR00777	5806	6948	4-AMINO-4-DEOXYCHORISMATE LYASE (EC 4.-.-.-)
707	708	RXA00106	GR00014	17469	17924	DIHYDROFOLATE REDUCTASE (EC 1.5.1.3)
709	710	RXN02198	VV0302	9228	11726	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
711	712	F RXA02198	GR00646	2483	6	5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
713	714	RXN02085	VV0126	8483	10717	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
715	716	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
717	718	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
719	720	RXN02648				5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
721	722	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
723	724	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14)
725	726	RXS02197				5-METHYLTETRAHYDROFOLATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.13)
727	728	RXC00988				PROTEIN INVOLVED IN FOLATE METABOLISM
729	730	RXC01518				MEMBRANE SPANNING PROTEIN INVOLVED IN FOLATE METABOLISM
731	732	RXC01942				ATP-BINDING PROTEIN INVOLVED IN FOLATE METABOLISM

### Molybdopterin Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
733	734	RXN02802	VV0112	17369	16299	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
735	736	F RXA02802	GR00783	7	474	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
737	738	F RXA00438	GR00103	362	796	MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN
739	740	RXN00437	VV0112	17824	17369	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
741	742	F RXA00437	GR00103	3	362	MOLYBDOPTERIN (MPT) CONVERTING FACTOR, SUBUNIT 2
743	744	RXN00439	VV0112	18742	18275	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
745	746	F RXA00439	GR00104	2	196	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
747	748	F RXA00442	GR00105	830	1087	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
749	750	RXA00440	GR00104	196	654	MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN CB
751	752	RXN00441	VV0112	19942	18779	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
753	754	F RXA00441	GR00105	2	793	MOLYBDOPTERIN CO-FACTOR SYNTHESIS PROTEIN
755	756	RXN02085				5-METHYLTETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
757	758	F RXA02085	GR00629	3496	5295	5-METHYLTETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
759	760	F RXA02086	GR00629	5252	5731	5-METHYLTETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
761	762	RXN02648				5-METHYLTETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
763	764	F RXA02648	GR00751	5254	4730	5-METHYLTETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
765	766	F RXA02658	GR00752	14764	15447	5-METHYLTETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE
						METHYLTRANSFERASE (EC 2.1.1.14)
767	768	RXA01516	GR00424	22360	22749	DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)
769	770	RXA01515	GR00424	21513	22364	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
771	772	RXA02024	GR00613	4026	4784	DIHYDROPTEROATE SYNTHASE (EC 2.5.1.15)
773	774	RXA01719	GR00488	1264	704	MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A
775	776	RXA01720	GR00488	2476	1268	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
777	778	RXS03223				MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
779	780	F RXA01970	GR00568	2	1207	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
781	782	RXA02629	GR00748	1274	690	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
783	784	RXA02318	GR00665	9684	9962	MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN
785	786	RXA01517	GR00424	22752	23228	(D90909) pterin-4a-carbinolamine dehydratase [Synecocystis sp.]
						2-AMINO-4-HYDROXY-6-HYDROXYMETHYLDIHYDROPTERIDINE
						PYRROPHOSPHOKINASE (EC 2.7.6.3)
787	788	RXN01304	VV0148	4449	4934	MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN
789	790	RXS02556				FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
791	792	RXS02560				OXYGEN-SENSITIVE NAD(P)H NITROREDUCTASE (EC 1.---) /
						DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
<b>Vitamin B<sub>12</sub>, porphyrins and heme metabolism</b>						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
793	794	RXA00382	GR00082	2752	1451	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8)
795	796	RXA00156	GR00023	10509	9400	FERROCHELATASE (EC 4.99.1.1)
797	798	RXA00624	GR00163	7910	8596	FERROCHELATASE (EC 4.99.1.1)
799	800	RXA00306	GR00051	2206	1274	HEMK PROTEIN
801	802	RXA00884	GR00242	10137	11276	OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.---)
803	804	RXN02503	VV0007	22456	22854	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
805	806	F RXA02503	GR00720	16906	17340	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
807	808	RXA00377	GR00081	1427	306	UROPORPHYRINOGEN DECARBOXYLASE (EC 4.1.1.37)
809	810	RXN02504	VV0007	22805	23362	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)
811	812	F RXA02504	GR00720	17379	17816	PORPHOBILINOGEN DEAMINASE (EC 4.3.1.8)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
813	814	RXN01162	VV0088	1849	524	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
815	816	F RXA01162	GR00330	1248	4	PRECORRIN-6Y METHYLASE (EC 2.1.1.-)
817	818	RXA01692	GR00474	1498	749	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107)
819	820	RXN00371	VV0226	4180	5973	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
821	822	F RXA00371	GR00078	929	6	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
823	824	F RXA00374	GR00079	1102	371	UROPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / UROPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
825	826	RXN00383	VV0223	4206	2863	PROTOPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / PROTOPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
827	828	F RXA00376	GR00081	287	6	PROTOPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / PROTOPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
829	830	RXN00383	GR00082	3876	2863	PROTOPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / PROTOPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
831	832	RXA01253	GR00365	2536	1787	PROTOPORPHYRIN-III C-METHYLTRANSFERASE (EC 2.1.1.107) / PROTOPORPHYRIN-III SYNTHASE (EC 4.2.1.75)
833	834	RXA02134	GR00639	1721	801	COBYRIC ACID SYNTHASE
835	836	RXA02135	GR00639	2809	1736	COBALAMIN (5'-PHOSPHATE) SYNTHASE
837	838	RXA02136	GR00639	3362	2841	NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.21)
839	840	RXN03114	VV0088	1	552	COBINAMIDE KINASE / COBINAMIDE PHOSPHATE GUANYLYLTRANSFERASE
841	842	RXN01810	VV0088	1739	663	COBG PROTEIN (EC 1.-.-.-)
843	844	RXS03205				HEMIN-BINDING PERIPLASMIC PROTEIN HMUT PRECURSOR
845	846	F RXA00306				HEMK PROTEIN
847	848	RXC01715				HEMK PROTEIN CYTOSOLIC PROTEIN INVOLVED IN PORPHYRIN METABOLISM

## Vitamin C precursors

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
849	850	RXN00420	VV0112	2511	1048	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
851	852	F RXA00420	GR00096	2	541	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
853	854	F RXA00426	GR00097	1737	2258	L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
855	856	RXN00708	VV0005	4678	3872	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
857	858	F RXA00708	GR00185	2030	1359	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
859	860	RXA02373	GR00688	1540	626	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-) oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)
861	862	RXS00389				ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
863	864	RXS00419				MEMBRANE SPANNING PROTEIN INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
865	866	RXC00416				OXIDOREDUCTASE INVOLVED IN METABOLISM OF VITAMIN C PRECURSORS
867	868	RXC02206				

  

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
869	870	RXS03074				S-ADENOSYLMETHIONINE-2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

## Vitamin K2

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
869	870	RXS03074				S-ADENOSYLMETHIONINE-2-DEMETHYLMENAQUINONE METHYLTRANSFERASE (EC 2.1.-.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
871	872	F RXA02906	GR10044	1142	645	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAUQUINONE METHYLTRANSFERASE (EC 2.1.-.-)
873	874	RXA02315	GR00665	8011	6383	2-SUCCINYL-6-HYDROXY-2,4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE /2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
875	876	RXA02319	GR00665	9977	10933	NAPHTHOATE SYNTHASE (EC 4.1.3.36)
877	878	RXS00393				1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
879	880	F RXA00393	GR00086	4030	4911	1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (EC 2.5.-.-)
881	882	RXA00391	GR00086	2031	2750	O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)
883	884	RXS02908				O-SUCCINYLBENZOIC ACID--COA LIGASE (EC 6.2.1.26)

  

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
885	886	RXA00997	GR00283	2389	1808	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
887	888	RXA02189	GR00642	986	249	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
889	890	RXA02311	GR00665	3073	2384	3-DEMETHYLBUBIQUINONE-9 3-METHYLTRANSFERASE (EC 2.1.1.64)
891	892	RXN02912	VV0135	13299	12547	UBIQUINONE/MENAUQUINONE BIOSYNTHESIS METHYLTRANSFERASE UBIE (EC 2.1.1.-)
893	894	RXS00998				COMA OPERON PROTEIN 2

  

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
895	896	RXA01215	GR00352	1187	213	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE, PRPP synthetase (EC 2.7.6.1)
897	898	RXN00558	VV0103	8235	9581	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
899	900	F RXA00558	GR00148	61	501	AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14)
901	902	RXN00626	VV0135	11624	10362	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
903	904	F RXA00629	GR00165	1450	1713	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13)
905	906	F RXA00626	GR00164	1	780	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE, GARS (EC 6.3.4.13)
907	908	RXA02623	GR00746	4875	4285	PHOSPHORIBOSYLFORMYLGLYCINAMIDE CYCLO-LIGASE (EC 6.3.3.1) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2)
909	910	RXA01442	GR00418	10277	9054	PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE 2 (EC 2.1.2.-)

## Ubiquinone biosynthesis

## Purines and Pyrimidines and other Nucleotides

### Regulation of purine and pyrimidine biosynthesis pathways

## Purine metabolism

### Purine Biosynthesis

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
911	912	RXN00537	VV0103	3351	5636	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
913	914	F RXA02805	GR00786	54	638	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
915	916	F RXA00537	GR00138	23	697	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
917	918	F RXA00561	GR00150	2	280	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
919	920	RXA00541	GR00139	2269	2937	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
921	922	RXA00520	GR00163	3049	3939	PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6)
923	924	RXN00770	VV0103	9614	10783	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
925	926	F RXA00557	GR00147	15	818	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
927	928	F RXA00770	GR00204	7809	7495	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1)
929	930	RXN02345	VV0078	4788	5984	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
931	932	F RXA02345	GR00676	1534	725	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (EC 4.1.1.21)
933	934	RXN02350	VV0078	8369	8863	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
935	936	F RXA02346	GR00677	127	5	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
937	938	F RXA02350	GR00678	1120	911	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT (EC 4.1.1.21)
939	940	RXA01087	GR00304	498	1373	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21)
941	942	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
943	944	RXA02622	GR00746	4274	2715	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE FORMYLTRANSFERASE (EC 2.1.2.3) / IMP CYCLOHYDROLASE (EC 3.5.4.10)

## GMP, GDP, AMP and ADP synthesis, from inosine-5'-monophosphate (IMP)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
945	946	RXN00488	VV0086	19066	20583	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
947	948	F RXA00492	GR00122	1171	1644	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
949	950	F RXA00488	GR00121	1	534	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
951	952	RXA02469	GR00715	1927	497	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
953	954	RXN00487	VV0086	23734	25302	GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.2)
955	956	F RXA00487	GR00120	712	2097	GMP SYNTHASE (EC 6.3.4.1)
957	958	RXA02237	GR00654	4577	5146	GUANYLATE KINASE (EC 2.7.4.8)
959	960	RXA01446	GR00418	17765	16476	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4)
961	962	RXA00619	GR00163	793	2220	ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
963	964	RXA00688	GR00179	10443	10985	ADENYLYL KINASE (EC 2.7.4.3)
965	966	RXA00266	GR00040	3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)

Table 1 (continued)

## GMP/AMP degrading activities

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.
967	968	RXA00489	GR00121
969	970	RXN02281	VV0152
971	972	F RXA02281	GR00659

## Pyrimidine metabolism

## Pyrimidine biosynthesis de novo:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.
973	974	RXA00147	GR00022
975	976	RXA00145	GR00022
977	978	RXA00146	GR00022
979	980	RXA02208	GR00647
981	982	RXA01660	GR00462
983	984	RXA02235	GR00654
985	986	RXN01892	VV0150
987	988	F RXA01892	GR00542
989	990	RXA00105	GR00014
991	992	RXA00131	GR00020
993	994	RXA00266	GR00040
995	996	RXA00718	GR00188
997	998	RXA01599	GR00447
999	1000	RXN02234	VV0134
1001	1002	F RXA02234	GR00654
1003	1004	RXN00450	VV0112
1005	1006	F RXA00450	GR00110
1007	1008	RXN02272	VV0020
1009	1010	F RXA02272	GR00655
1011	1012	RXN03004	VV0237
1013	1014	RXN03137	VV0129
1015	1016	RXN03171	VV0328
1017	1018	F RXA02857	GR10003

NT Start	NT Stop	Function
654	1775	GMP REDUCTASE (EC 1.6.6.8)
1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)

  

NT Start	NT Stop	Function
9722	10900	CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (EC 6.3.5.5)
7258	8193	ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN (EC 2.1.3.2)
8249	9589	DIHYDROOROTASE (EC 3.5.2.3)
2	1003	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1)
591	1142	OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10)
3207	4040	OROTIDINE 5'-PHOSPHATE DECARBOXYLASE (EC 4.1.1.23)
3020	3748	URIDYLATE KINASE (EC 2.7.4.-)
47	775	URIDYLATE KINASE (EC 2.7.4.-)
16672	17346	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
7621	7013	THYMIDYLATE KINASE (EC 2.7.4.9)
3769	3362	NUCLEOSIDE DIPHOSPHATE KINASE (EC 2.7.4.6)
4576	5283	CYTIDYLATE KINASE (EC 2.7.4.14)
8780	10441	CTP SYNTHASE (EC 6.3.4.2)
24708	28046	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
1	3198	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (EC 6.3.5.5)
34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
15566	16810	CYTOSINE DEAMINASE (EC 3.5.4.1)
6691	7935	CREATININE DEAMINASE (EC 3.5.4.21)
1862	2341	DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
9680	9579	THYMIDYLATE SYNTHASE (EC 2.1.1.45)
568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)

Table 1 (continued)

Purine and pyrimidine base, nucleoside and nucleotide salvage, interconversion, reduction and degradation:  
Purines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
1019	1020	RXA02771	GR00772	1329	1883	ADENINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.7)
1021	1022	RXA01512	GR00424	17633	18232	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8)
1023	1024	RXA02031	GR00618	3820	3347	XANTHINE GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.22)
1025	1026	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1027	1028	RXN02772	VW0171	2045	1011	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1029	1030	F RXA02772	GR00772	1962	2741	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1031	1032	F RXA02773	GR00772	2741	2902	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1033	1034	RXA01835	GR00517	3147	3677	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1035	1036	RXA01483	GR00422	19511	18240	DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (EC 3.1.5.1)
1037	1038	RXN01027	VW0143	5761	6768	DIADENOSINE 5',5''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1039	1040	F RXA01024	GR00293	661	5	DIADENOSINE 5',5''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1041	1042	RXA01027	GR00294	2580	2347	DIADENOSINE 5',5''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1043	1044	RXA01528	GR00425	5653	5126	DIADENOSINE 5',5''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
1045	1046	RXA00072	GR00012	446	6	PHOSPHADENOSINE PHOSPHOSULFATE REDUCTASE (EC 1.8.99.4)
1047	1048	RXA01878	GR00537	1239	2117	DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-)
1049	1050	RXN02281	VW0152	1893	3323	AMP NUCLEOSIDASE (EC 3.2.2.4)
1051	1052	F RXA02281	GR00659	1101	34	AMP NUCLEOSIDASE (EC 3.2.2.4)
1053	1054	RXN01240	VW0090	30442	29420	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
1055	1056	RXN02008	VW0171	1138	5	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
1057	1058	RXN01940	VW0120	10268	9333	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1059	1060	F RXA01940	GR00557	3	581	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1061	1062	RXA02559	GR00731	5418	6320	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1063	1064	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
1065	1066	RXN01079	VW0084	38084	35982	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1067	1068	F RXA01079	GR00301	693	4	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1069	1070	F RXA01084	GR00302	3402	2062	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1071	1072	RXN01920	VW0084	32843	31842	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (EC 1.17.4.1)
1073	1074	F RXA01920	GR00550	1321	908	RIBONUCLEOTIDE REDUCTASE SUBUNIT R2F
1075	1076	RXA01080	GR00301	1240	797	NRDI PROTEIN
1077	1078	RXA00867	GR00237	1	627	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1079	1080	RXA01416	GR00413	2	631	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)
1081	1082	RXA01486	GR00423	660	4	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8)

Pyrimidine and purine metabolism:

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1083	1084	RXA01678	GR00467	7162	7689	2'-3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1085	1086	RXA01679	GR00467	7729	8964	2'-3'-CYCLIC-NUCLEOTIDE 2'-PHOSPHODIESTERASE (EC 3.1.4.16)
1087	1088	RXN01488	VV0139	39842	40789	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
1089	1090	RXC00540				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1091	1092	RXC00560				PROTEIN INVOLVED IN PURINE METABOLISM
1093	1094	RXC01088				CYTOSOLIC PROTEIN INVOLVED IN PURINE METABOLISM
1095	1096	RXC02624				MEMBRANE SPANNING PROTEIN INVOLVED IN PURINE METABOLISM
1097	1098	RXC02665				PROTEIN INVOLVED IN PURINE METABOLISM
1099	1100	RXC02770				LIPOPROTEIN INVOLVED IN PURINE METABOLISM
1101	1102	RXC02238				PROTEIN INVOLVED IN METABOLISM OF S-ADENOSYLMETHIONINE, PURINES AND PANTOTHENATE
1103	1104	RXC01946				ABC TRANSPORTER ATP-BINDING PROTEIN INVOLVED IN PURINE METABOLISM

## Pyrimidines:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1105	1106	RXN03171	VV0328	568	1080	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1107	1108	F RXA02857	GR10003	570	1082	URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1109	1110	RXN00450	VV0112	34491	34814	CYTOSINE DEAMINASE (EC 3.5.4.1)
1111	1112	F RXA00450	GR00110	322	5	CYTOSINE DEAMINASE (EC 3.5.4.1)
1113	1114	RXA00465	GR00117	337	828	CYTOSINE DEAMINASE (EC 3.5.4.1)
1115	1116	RXA00717	GR00188	3617	4576	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70)
1117	1118	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41)
1119	1120	RXA02536	GR00726	8581	7826	BETA-UREIDOPROPIONASE (EC 3.5.1.6)
1121	1122	RXN01209	VV0270	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1123	1124	F RXA01209	GR00348	1019	2446	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1125	1126	RXN01617	VV0050	22187	22858	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1127	1128	F RXA01617	GR00451	2	616	PHOSPHOMETHYLPYRIMIDINE KINASE (EC 2.7.4.7)
1129	1130	RXC01600				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1131	1132	RXC01622				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1133	1134	RXC00128				EXPORTED PROTEIN INVOLVED IN METABOLISM OF PYRIDINES AND ADENOSYLMOCYSTEINE
1135	1136	RXC01709				CYTOSOLIC PROTEIN INVOLVED IN PYRIMIDINE METABOLISM
1137	1138	RXC02207				EXPORTED PROTEIN INVOLVED IN PYRIMIDINE METABOLISM

Table 1 (continued)

Sugars						
Trehalose						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1139	1140	RXA00347	GR00065	246	1013	TREHALOSE-PHOSPHATASE (EC 3.1.3.12)
1141	1142	RXN01239	VV0090	32921	30489	maltooligosyltrehalose synthase
1143	1144	F RXA01239	GR00358	5147	7579	maltooligosyltrehalose synthase
1145	1146	RXA02645	GR00751	714	2543	maltooligosyltrehalose trehalohydrolase
1147	1148	RXN02355	VV0051	735	4	TREHALOSE/MALTOSE BINDING PROTEIN
1149	1150	RXN02909	VV0135	38532	39017	Hypothetical Trehalose-Binding Protein
1151	1152	RXS00349				Hypothetical Trehalose Transport Protein
1153	1154	RXS03183				TREHALOSE/MALTOSE BINDING PROTEIN
1155	1156	RXC00874				TRANSMEBRANE PROTEIN INVOLVED IN TREHALOSE METABOLISM

TABLE 2 - Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from corynebacterium bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Corynebacterium bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	glbB; gltD	Glutamine :oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651			
AF041436	argK	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquininate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

		ectP	Transport of proline	of ectoine, glycine betaine,	
AJ001436	ectP				Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD		Tetrahydrodipicolinate (incomplete)		Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA		Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase		
AJ010319	fisY, glnB, glnD; srp; amtP		Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein		Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat		Chloramphenicol acetyl transferase		
AJ224946	mgo		L-malate: quinone oxidoreductase		Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh		NADH dehydrogenase		
AJ238703	porA		Porin		Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429			Transposase element IS31831		Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA		2-oxoglutarate dehydrogenase		Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh, hk		Homoserine dehydrogenase; homoserine kinase		Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359			Upstream of kinase gene		Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375			Tryptophan operon		
E01376	trpL; trpE		Leader peptide; anthranilate synthase		Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

	Promoter and operator regions of tryptophan operon	
E01377		Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

		Mutated aspartokinase alpha subunit	
E06827			Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membrane protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jeften, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
L35906	dtxR	Diphtheria toxin repressor	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M13774		Prephenate dehydratase	Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16175	5S rRNA		Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16663	trpE	Anthrnilate synthase, 5' end	
M16664	trpA	Tryptophan synthase, 3' end	

Table 2 (continued)

			Phosphoenolpyruvate carboxylase	
M25819				O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106			23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108			23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	accD; brnQ; yhbW		Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminothylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp		Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD		Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIR		Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA			
U31224	ppx			Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC		L-proline: ADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh		?gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

	bioB	Biotin synthase	
U31281			Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thiR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'-5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i> ,
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda dacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)

Table 2 (continued)

Table 2 (continued)				
X55994	trpL, trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)	
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)	
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda corynebacteriophage," <i>FEBS Microbiol. Lett.</i> , 66:299-302 (1990)	
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)	
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)	
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)	
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)	
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)	
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)	
X67737	dapB	Dihydrodipicolinate reductase		
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)	
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)	

Table 2 (continued)

	leuA	Isopropylmalate synthase	
X70959			Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mitrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pia-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

X82061	16S rDNA	16S ribosomal RNA				Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?				Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase				Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA				Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?				Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5901-5903 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase				Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase				Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site				Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting <i>Arthrobacter aureus</i> C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1				Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2				Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10				Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13				Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360	Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

Table 2 (continued)				
X96580	panB, panC, xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)	
X96962		Insertion sequence IS1207 and transposase		
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)	
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)	
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.13)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)	
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)	
Y00546	hom, thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)	
Y08964	murC, fisQ/divD; fisZ	UDP-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the fisZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)	
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)	
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)	
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)	
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)	
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)	

Table 2 (continued)

	glnA	Glutamine synthetase I	
Y13221			Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site <i>Corynebacterium</i> 304L	Moreau, S. et al. "Analysis of the integration functions of &phi;304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniagenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							
<i>Brevibacterium</i>	<i>flavum</i>			B11477					
<i>Brevibacterium</i>	<i>flavum</i>			B11478					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>healii</i>	15527							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21004							
<i>Brevibacterium</i>	<i>ketoglutamicum</i>	21089							
<i>Brevibacterium</i>	<i>ketosoreductum</i>	21914							
<i>Brevibacterium</i>	<i>lactofermentum</i>				70				
<i>Brevibacterium</i>	<i>lactofermentum</i>				74				
<i>Brevibacterium</i>	<i>lactofermentum</i>				77				
<i>Brevibacterium</i>	<i>lactofermentum</i>	21798							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21799							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21800							
<i>Brevibacterium</i>	<i>lactofermentum</i>	21801							
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11470					
<i>Brevibacterium</i>	<i>lactofermentum</i>			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniogenes	6872						2399	
Corynebacterium	ammoniogenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4<sup>th</sup> edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx000023	3579	GB_EST33.A1776129	483	A1776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence	Lycopersicon esculentum	40,956	29-Jun-99
		GB_EST33.A1776129	483	A1776129	EST257217 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER17D3, mRNA sequence	Lycopersicon esculentum	40,956	29-Jun-99
rx000044	1059	EM_PAT.E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	42,979	08-OCT- 1997 (Rel 52, Created)
		GB_PAT.126124	6911	126124	Sequence 4 from patent US 5556776.	Unknown.	42,979	07-OCT- 1996
		GB_BA2.ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	39,097	17-DEC- 1993
rx000064	1401	GB_PAT.E16763	2517	E16763	gDNA encoding aspartate transferase (AAT).	Corynebacterium glutamicum	95,429	28-Jul-99
		GB_HTG2.AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02 O 3 map 99B-99B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces	Drosophila melanogaster	31,111	2-Aug-99
rx000072		GB_HTG2.AC007892	134257	AC007892	Drosophila melanogaster chromosome 3 clone BACR02003 (D797) RPCI-98 02 O 3 map 99B-99B strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces	Drosophila melanogaster	31,111	2-Aug-99
rx000105	798	GB_BA1.MTV002	56414	AL008957	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162	Mycobacterium tuberculosis	37,753	17-Jun-98
		GB_BA1.ECU29581	71128	U29581	Escherichia coli K-12 genome, approximately 63 to 64 minutes.	Escherichia coli	35,669	14-Jan-97
		GB_BA2.AE000366	10405	AE000366	Escherichia coli K-12 MG1655 section 256 of 400 of the complete genome.	Escherichia coli	35,669	12-Nov-98
rx000106	579	GB_EST15.AA494237	367	AA494237	ng83f04.s1 NCI_CGAP_Pf6 Homo sapiens cDNA clone IMAGE 941407 similar to SW.DYR_LACCA P00381 DIHYDROFOLATE REDUCTASE mRNA sequence	Homo sapiens	42,896	20-Aug-97
		GB_BA2.AF161327	2021	AF161327	Corynebacterium diphtheriae histidine kinase ChrS (chrS) and response regulator ChrA (chrA) genes, complete cds	Corynebacterium diphtheriae	40,210	9-Sep-99
		GB_PAT.AR041189	654	AR041189	Sequence 4 from patent US 5811286.	Unknown.	41,176	29-Sep-99
rx000115	1170	GB_PR4.AC007110	148336	AC007110	Homo sapiens chromosome 17, clone hRPK 472_J_18, complete sequence.	Homo sapiens	36,783	30-MAR- 1999
		GB_HTG3.AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces	Homo sapiens	40,296	2-Sep-99
		GB_HTG3.AC008537	170030	AC008537	Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces	Homo sapiens	40,296	2-Sep-99

Table 4 (continued)

rx00116	1284	GB_BA2:AF062345	16458	AF062345	Caulobacter crescentus Sst1 (sst1), S-layer protein subunit (rsaA), ABC transporter (rsaD), membrane forming unit (rsaE), putative GDP-mannose-4,6-dehydratase (lpsA), putative acetyltransferase (lpsB), putative perosamine synthetase (lpsC), putative mannosyltransferase (lpsD), putative mannosyltransferase (lpsE), outer membrane protein (rsaF), and putative perosamine transferase (lpsE) genes, complete cds. Sequence 6 from patent US 5500353.	Caulobacter crescentus	36,235	19-OCT-1999
		GB_PAT:118647	3300	118647		Unknown.	36,821	07-OCT-1996
		GB_GSS13:AQ44619	751	AQ446197	nbxb0062D16r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0062D16r, genomic survey sequence.	Oryza sativa	38,124	8-Apr-99
rx00131	732	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	43,571	17-Jun-98
		GB_BA1:SAR7932	15176	AJ007932	Streptomyces argillaceus mithramycin biosynthetic genes.	Streptomyces argillaceus	41,116	15-Jun-99
		GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	39,726	17-Jun-98
rx00132	1557	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,788	17-Jun-98
		GB_IN2:TVU40872	1882	U40872	Trichomonas vaginalis S-adenosyl-L-homocysteine hydrolase gene, complete cds.	Trichomonas vaginalis	61,914	31-OCT-1996
		GB_HTG6:AC010706	169265	AC010706	Drosophila melanogaster chromosome X clone BACR36D15 (D887) RPC1-98 36.D.15 map 13C-13E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 74 unordered pieces.	Drosophila melanogaster	51,325	22-Nov-99
rx00145	1059	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	63,365	18-Jun-98
		GB_BA1:PSEPYRBX	2273	L19649	Pseudomonas aeruginosa aspartate transcarbamoylase (pyrB) and dihydroorotase-like (pyrX) genes, complete cds's.	Pseudomonas aeruginosa	56,080	26-Jul-93
		GB_BA1:LLPYRBDNA	1468	X84262	L. leichmannii pyrB gene.	Lactobacillus leichmannii	47,514	29-Apr-97
rx00146	1464	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	60,714	18-Jun-98
		GB_BA1:MTCV154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	39,229	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	36,618	03-DEC-1996
rx00147	1302	GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	61,527	18-Jun-98
		GB_BA1:MSGB937C	38914	L78820	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	59,538	15-Jun-96
		GB_BA1:PAU81259	7285	U81259	Pseudomonas aeruginosa dihydrodipicolinate reductase (dapB) gene, partial cds, carbamoylphosphate synthetase small subunit (carA) and carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FisJ homolog (ftsJ) gene, partial cds.	Pseudomonas aeruginosa	55,396	23-DEC-1996
rx00156	1233	GB_BA1:SC9B10	33320	AL009204	Streptomyces coelicolor cosmid 9B10	Streptomyces coelicolor	52,666	10-Feb-99

Table 4 (continued)

GB_BA2 AF002133	15437	AF002 33	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	54,191	26-MAR-1998
GB_BA1 D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds.	Propionibacterium freudenreichii	46,667	6-Feb-99
GB_HTG3 AC008167	174223	AC008 67	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
GB_HTG3 AC008167	174223	AC008 67	Homo sapiens clone NH0172013, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	37,451	21-Aug-99
GB_HTG4 AC010118	80605	AC010 18	Drosophila melanogaster chromosome 3L/62B1 clone RPC198-10D15, *** SEQUENCING IN PROGRESS ***; 51 unordered pieces.	Drosophila melanogaster	38,627	16-OCT-1999
GB_BA1 AB024708	8734	AB024 708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	92,113	13-MAR-1999
GB_BA1 AB024708	8734	AB024 708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	93,702	13-MAR-1999
GB_EST24 AI232702	528	AI2327 2	EST229390 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKICF35 3' end, mRNA sequence.	Rattus sp	34,221	31-Jan-99
GB_HTG2 HSDJ850E	117353	AL121758 9	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
GB_HTG2 HSDJ850E	117353	AL121758 9	Homo sapiens chromosome 20 clone RP5-850E9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	37,965	03-DEC-1999
GB_PR2 CNS01DSA	159400	AL121756	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-412H8 of RPC1-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	38,796	11-Nov-99
GB_HTG2 AC005079	110000	AC005079 0	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
GB_HTG2 AC005079	110000	AC005079 1	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
GB_HTG2 AC005079	110000	AC005079 1	Homo sapiens clone RG252P22, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	38,227	22-Nov-98
GB_BA1 PPEA3NIF	19771	X99694	Plasmid pEA3 nitrogen fixation genes	Enterobacter agglomerans	48,826	2-Aug-96
GB_BA2 AF128444	2477	AF1284 4	Rhodobacter capsulatus molybdenum cofactor biosynthetic gene cluster, partial sequence.	Rhodobacter capsulatus	40,135	22-MAR-1999
GB_HTG4 AC010111	138938	AC0101 1	Drosophila melanogaster chromosome 3L/70C1 clone RPC198-9B18, *** SEQUENCING IN PROGRESS ***; 64 unordered pieces.	Drosophila melanogaster	39,527	16-OCT-1999
GB_BA2 AF124518	1758	AF1245 8	Corynebacterium glutamicum 3-dehydroquinase (aroD) and shikimate dehydrogenase (aroE) genes, complete cds.	Corynebacterium glutamicum	98,237	18-MAY-1999
GB_PR3 AC004593	150221	AC0045 3	Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.	Homo sapiens	36,616	18-Apr-98
GB_HTG2 AC006907	188972	AC0069 7	Caenorhabditis elegans clone Y76B12, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces.	Caenorhabditis elegans	37,095	26-Feb-99
GB_BA1 CGLYSI	4232	X60312	C.glutamicum lysI gene for L-lysine permease.	Corynebacterium glutamicum	100,000	30-Jan-92

Table 4 (continued)

GB_HTG1:PFMAL13P 192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
GB_HTG1:PFMAL13P 192581	AL049180	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	34,947	11-Aug-99
GB_IN2:EHU89655 3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	36,496	23-MAY-1997
GB_IN2:EHU89655 3219	U89655	Entamoeba histolytica unconventional myosin IB mRNA, complete cds.	Entamoeba histolytica	37,544	23-MAY-1997
GB_RO:AF016190 2939	AF016190	Mus musculus connexin-36 (Cx36) gene, complete cds.	Mus musculus	41,856	9-Feb-99
EM_PAT:E09719 3505	E09719	DNA encoding precursor protein of alkaline cellulase.	Bacillus sp.	34,741	08-OCT-1997 (Rel. 52, Created)
GB_PAT:E02133 3494	E02133	gDNA encoding alkaline cellulase.	Bacillus sp.	34,741	29-Sep-97
GB_IN1:CELK05F6 36912	AF040653	Caenorhabditis elegans cosmid K05F6.	Caenorhabditis elegans	36,943	6-Jan-98
GB_BA1:CGU43535 2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	36,658	9-Apr-97
GB_RO:RNU30789 3510	U30789	Rattus norvegicus clone N27 mRNA.	Rattus norvegicus	38,190	20-Aug-96
GB_BA2:CGU31281 1614	U31281	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds.	Corynebacterium glutamicum	99,111	21-Nov-96
GB_BA1:BRLBIOBA 1647	D14084	Brevibacterium flavum gene for biotin synthetase, complete cds.	Corynebacterium glutamicum	98,489	3-Feb-99
GB_PAT:E03937 1005	E03937	DNA sequence encoding Brevibacterium flavum biotin-synthase.	Corynebacterium glutamicum	98,207	29-Sep-97
GB_BA1:MTCY427 38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome, segment 99/162.	Mycobacterium tuberculosis	35,615	24-Jun-99
GB_BA1:MSGB32CS 36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	60,917	15-Jun-96
GB_BA1:MTCY427 38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome, segment 99/162.	Mycobacterium tuberculosis	44,606	24-Jun-99
GB_BA1:MSGB32CS 36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	52,516	15-Jun-96
GB_BA1:MTCY427 38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome, segment 99/162.	Mycobacterium tuberculosis	38,079	24-Jun-99
GB_OM:BOVELA 3242	J02717	Bovine elastin a mRNA, complete cds.	Bos taurus	39,351	27-Apr-93
GB_BA1:CGTHRC 3120	X56037	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2).	Corynebacterium glutamicum	99,808	17-Jun-97
GB_PAT:J09078 3146	J09078	Sequence 4 from Patent WO 8809819.	Unknown.	99,617	02-DEC-1994
GB_BA1:BLTHRESY 1892	Z29563	Brevibacterium lactofermentum, ATCC 13869, DNA (genomic).	Corynebacterium glutamicum	99,170	20-Sep-95
GB_BA1:CGGLNA 3686	Y13221	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	100,000	28-Aug-97

GB_BA2	AF005635	1690	AF005635	Corynebacterium glutamicum glutamine synthetase (glnA) gene, complete cds.	Corynebacterium glutamicum	98,906	14-Jun-99
GB_BA1	MSG827CS	38793	L78817	Mycobacterium leprae cosmid B27 DNA sequence.	Mycobacterium leprae	66,345	15-Jun-96
GB_EST27	AI455217	624	AI45527	LD21828 3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD21828 3prime, mRNA sequence	Drosophila melanogaster	34,510	09-MAR-1999
GB_BA2	SSU30252	2891	U30252	Synechococcus PCC7942 nucleoside diphosphate kinase and ORF2 protein genes, complete cds, ORF1 protein gene, partial cds, and neutral site I for vector use.	Synechococcus PCC7942	37,084	29-OCT-1999
GB_EST21	AA911262	581	AA911262	oe75a02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1417418 3' similar to gb A18757 UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR, GPI-ANCHORED (HUMAN)., mRNA sequence.	Homo sapiens	37,500	21-Apr-98
GB_BA1	MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	52,972	09-MAR-1995
GB_IN2	AC004373	72722	AC004373	Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.	Drosophila melanogaster	46,341	17-Jul-98
GB_IN2	AF145653	3197	AF145653	Drosophila melanogaster clone GH08860 BcDNA GH08860 (BcDNA GH08860) mRNA, complete cds	Drosophila melanogaster	49,471	14-Jun-99
GB_BA1	AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	96,556	13-MAR-1999
GB_BA1	MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome, segment 159/162.	Mycobacterium tuberculosis	39,496	17-Jun-98
GB_BA1	SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,946	16-Aug-99
GB_BA1	AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,374	13-MAR-1999
GB_BA1	MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome, segment 159/162.	Mycobacterium tuberculosis	41,333	17-Jun-98
GB_BA1	SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,554	16-Aug-99
GB_BA1	AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds.	Corynebacterium glutamicum	99,312	13-MAR-1999
GB_BA1	MTCY1A6	37751	Z83864	Mycobacterium tuberculosis H37Rv complete genome, segment 159/162.	Mycobacterium tuberculosis	36,971	17-Jun-98
GB_BA1	SC3A3	15901	AL109849	Streptomyces coelicolor cosmid 3A3.	Streptomyces coelicolor A3(2)	37,905	16-Aug-99
GB_VI	SBVORFS	7568	M89923	Sugarcanne bacilliform virus ORF 1,2, and 3 DNA, complete cds	Sugarcanne bacilliform virus A3(2)	35,843	12-Jun-93
GB_EST37	AI967505	380	AI967505	Ljirnpes103-215-c10 Ljirnp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence	Lotus japonicus	42,593	24-Aug-99
GB_IN1	CELK09H9	37881	AF043700	Caenorhabditis elegans cosmid K09H9	Caenorhabditis elegans	34,295	22-Jan-98

Table 4 (continued)

rx00377	1245	GB_BA1.CCU13664	1678	U13664	Caulobacter crescentus uroporphyrinogen decarboxylase homolog (hemE) gene, partial cds.	Caulobacter crescentus	36,832	24-MAR-1995
		GB_PL1.ANSDGENE	1299	Y08866	A. nidulans sD gene.	Emericella nidulans	39,603	17-OCT-1996
rx00382	1425	GB_GSS4.AQ730303	483	AQ730303	HS_5505_B1_C04_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=7 Row=F, genomic survey sequence	Homo sapiens	36,728	15-Jul-99
		GB_BA1.PAHEML	4444	X82072	P. aeruginosa hemL gene.	Pseudomonas aeruginosa	54,175	18-DEC-1995
		GB_BA1.MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	61,143	17-Jun-98
		GB_BA1.MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	61,143	03-DEC-1996
rx00383	1467	GB_BA1.MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	43,981	27-Aug-99
		GB_HTG2.AC006269	167171	AC006269	Homo sapiens chromosome 17 clone hRPK.515_E_23 map 17, ... SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	35,444	10-Jun-99
		GB_HTG2.AC007638	178053	AC007638	Homo sapiens chromosome 17 clone hRPK.515_O_17 map 17, ... SEQUENCING IN PROGRESS ***; 8 unordered pieces.	Homo sapiens	34,821	22-MAY-1999
rx00391	843	GB_EST38.AW01705	613	AW017053	Schistosoma mansoni cDNA clone SMMAS14 5' end, mRNA sequence.	Schistosoma mansoni	40,472	10-Sep-99
		GB_PAT.AR065852	32207	AR065852	Sequence 20 from patent US 5849564.	Unknown	38,586	29-Sep-99
		GB_VI.AF148805	28559	AF148805	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds, and ORF 69; kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds.	Kaposi's sarcoma-associated herpesvirus	38,509	2-Aug-99
rx00393	1017	GB_BA1.MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,308	17-Jun-98
		GB_BA1.MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	39,282	03-DEC-1996
rx00402	623	GB_BA1.MLB1306	7762	Y13803	Mycobacterium leprae cosmid B1306 DNA.	Mycobacterium leprae	39,228	24-Jun-97
		GB_BA2.AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,672	19-MAR-1998
		GB_BA2.AF109162	4514	AF109162	Corynebacterium diphtheriae heme uptake locus, complete sequence	Corynebacterium diphtheriae	40,830	8-Jun-99
		GB_BA2.AF092918	20758	AF092918	Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.	Pseudomonas alcaligenes	50,161	06-DEC-1998
rx00403	1254	GB_BA2.AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds.	Corynebacterium glutamicum	99,920	19-MAR-1998
		GB_BA1.MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	52,898	23-Jun-99
		GB_EST23.AL111288	750	AL111288	SWOVAMCAQ02A05SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOVAMCAQ02A05 5' mRNA sequence.	Onchocerca volvulus	37,565	31-Aug-98

Table 4 (continued)

rx00405	613	GB_BA1.MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162	Mycobacterium tuberculosis	57,259	23-Jun-99
		GB_PR4.AC005145	143678	AC005145	Homo sapiens Xp22-166-169 GSHB-523A23 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	34,179	08-DEC-1998
		GB_BA1.MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162	Mycobacterium tuberculosis	40,169	23-Jun-99
rx00420	1587	GB_BA1.MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162	Mycobacterium tuberculosis	62,031	17-Jun-98
		GB_BA1.MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126	Mycobacterium tuberculosis	61,902	10-DEC-1996
		GB_BA1.MSGB971C <sub>S</sub>	37566	L78821	Mycobacterium leprae cosmid B971 DNA sequence.	Mycobacterium tuberculosis	39,651	15-Jun-96
rx00435	1296	GB_BA1.AFACBBTZ	2760	M68904	Alcaligenes eutrophus chromosomal transketolase (cbbTc) and phosphoglycolate phosphatase (cbbZc) genes, complete cds	Ralstonia eutropha	38,677	27-Jul-94
		GB_HTG4.AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
		GB_HTG4.AC009541	169583	AC009541	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 25 unordered pieces.	Homo sapiens	36,335	12-OCT-1999
rx00437	579	GB_PR4.AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK 372_K_20, complete sequence.	Homo sapiens	31,738	18-Nov-98
		GB_BA1.SC2A11	22789	AL031184	Streptomyces coelicolor cosmid 2A11	Streptomyces coelicolor	43,262	5-Aug-98
		GB_PR4.AC005951	155450	AC005951	Homo sapiens chromosome 17, clone hRPK 372_K_20, complete sequence.	Homo sapiens	37,647	18-Nov-98
rx00439	591	GB_BA1.MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	37,088	23-Jun-99
		GB_PL2.AF167358	1022	AF167358	Rumex acetosa expansin (EXP3) gene, partial cds	Rumex acetosa	46,538	17-Aug-99
		GB_HTG3.AC009120	269445	AC009120	Homo sapiens chromosome 16 clone RPCI-11_484E3, *** SEQUENCING IN PROGRESS ***; 34 unordered pieces.	Homo sapiens	43,276	3-Aug-99
rx00440	582	GB_BA2.SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames.	Streptomyces lividans	43,080	27-OCT-1999
		GB_BA1.SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1	Streptomyces coelicolor	42,931	4-Jun-98
		GB_BA1.SC2E1	38962	AL023797	Streptomyces coelicolor cosmid 2E1	Streptomyces coelicolor	36,702	4-Jun-98
rx00441	1287	GB_PR2.HS173D1	117338	AL031984	Human DNA sequence from clone 173D1 on chromosome 1p36.21-36.33 Contains ESTs, STSs and GSSs, complete sequence.	Homo sapiens	38,027	23-Nov-99
		GB_HTG2.HSDJ719K	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
		GB_HTG2.HSDJ719K <sub>3</sub>	267114	AL109931	Homo sapiens chromosome X clone RP4-719K3 map q21.1-21.31, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,521	03-DEC-1999
rx00446	987	GB_BA1.SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78	Streptomyces coelicolor	56,410	26-Nov-98
		GB_HTG4.AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***; 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999
		GB_HTG4.AC009367	226055	AC009367	Drosophila melanogaster chromosome 3L/76A2 clone RPCI98-48B15, *** SEQUENCING IN PROGRESS ***; 44 unordered pieces.	Drosophila melanogaster	34,959	16-OCT-1999

Table 4 (continued)

rx00448	1143	GB_PR3 AC003670	88945	AC003670	Homo sapiens 12q13.1 PAC RPC11-130F5 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	35,682	9-Jun-98
		GB_HTG2 AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS *** 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
		GB_HTG2 AF029367	148676	AF029367	Homo sapiens chromosome 12 clone RPC1-1 130F5 map 12q13.1, *** SEQUENCING IN PROGRESS *** 156 unordered pieces.	Homo sapiens	31,373	18-OCT-1997
rx00450	424	GB_HTG2 AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPC1-98 02.L.16 map 89E-90A strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_HTG2 AC007824	133361	AC007824	Drosophila melanogaster chromosome 3 clone BACR02L16 (D715) RPC1-98 02.L.16 map 89E-90A strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** 91 unordered pieces.	Drosophila melanogaster	40,000	2-Aug-99
		GB_EST35 A1818057	412	A1818057	3' similar to gb: Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	35,714	24-Aug-99
rx00461	975	GB_BA1 MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	39,308	8-Aug-97
		GB_IN1 DMC86E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4.	Drosophila melanogaster	37,487	27-Apr-99
		GB_GSS15 AQ64032	467	AQ640325	927P1-2H3.TP 927P1 Trypanosoma brucei genomic clone 927P1-2H3, genomic survey sequence.	Trypanosoma brucei	38,116	8-Jul-99
rx00465								
rx00487	1692	GB_BA1 BAGUAA	3866	Y10499	B. ammoniagenes guaA gene.	Corynebacterium ammoniagenes	74,259	8-Jan-98
		GB_BA2 U00015	42325	U00015	Mycobacterium leprae cosmid B1620	Mycobacterium leprae	37,248	01-MAR-1994
		GB_BA1 MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome, segment 145/162.	Mycobacterium tuberculosis	39,725	17-Jun-98
rx00488	1641	GB_BA1 MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome, segment 145/162.	Mycobacterium tuberculosis	39,451	17-Jun-98
		GB_BA2 U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	39,178	01-MAR-1994
rx00489	1245	GB_BA1 SCAJ10601	4692	AJ010601	Streptomyces coelicolor A3(2) DNA for whiD and whiK loci.	Streptomyces coelicolor	60,835	17-Sep-98
		GB_BA2 U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,041	01-MAR-1994
		GB_HTG2 HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
		GB_HTG2 HS225E12	126464	AL031772	Homo sapiens chromosome 6 clone RP1-225E12 map q24, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	36,756	03-DEC-1999
rx00533	1155	GB_BA1 CGLYS	2803	X57226	C. glutamicum lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,913	17-Feb-97

Table 4 (continued)

GB_BA1 CGCYSCAS	1591	X82928	Corynebacterium aspartate-semialdehyde dehydrogenase gene.	Corynebacterium glutamicum	99,221	17-Feb-97
GB_PAT A07546	2112	A07546	Recombinant DNA fragment (PstII-XhoI).	synthetic construct	99,391	30-Jul-93
GB_BA1 CGLYS	2803	X57226	Corynebacterium lysC-alpha, lysC-beta and asd genes for aspartokinase-alpha and -beta subunits, and aspartate beta semialdehyde dehydrogenase, respectively (EC 2.7.2.4; EC 1.2.1.11).	Corynebacterium glutamicum	99,856	17-Feb-97
GB_BA1 CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds.	Corynebacterium flavescens	98,701	11-Jun-93
GB_PAT E14514	1643	E14514	DNA encoding Brevibacterium aspartokinase.	Corynebacterium glutamicum	98,773	28-Jul-99
GB_BA1 CGLEUA	3492	X70959	Corynebacterium gene leuA for isopropylmalate synthase.	Corynebacterium glutamicum	100,000	10-Feb-99
GB_BA1 MTU025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162.	Mycobacterium glutamicum	68,003	24-Jun-99
GB_BA1 MTU88526	2412	U88526	Mycobacterium tuberculosis putative alpha-isopropyl malate synthase (leuA) gene, complete cds.	tuberculosis	68,185	26-Feb-97
GB_BA2 SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	tuberculosis	63,187	21-Sep-99
GB_BA1 MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome, segment 39/162.	A3(2)	62,401	17-Jun-98
GB_BA1 MTU34956	2462	U34956	Mycobacterium tuberculosis phosphoribosylformylglycinamide synthase (furL) gene, complete cds.	Mycobacterium tuberculosis	62,205	28-Jan-97
GB_PAT I92052	2115	I92052	Sequence 19 from patent US 5726299.	Unknown.	98,359	01-DEC-1998
GB_BA1 MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	62,468	24-Jun-97
GB_BA1 MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome, segment 36/162.	Mycobacterium tuberculosis	60,814	17-Jun-98
GB_BA1 BAPURF	1885	X91252	B. ammoniagenes purF gene.	Corynebacterium ammoniagenes	66,095	5-Jun-97
GB_BA1 MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	64,315	09-MAR-1995
GB_BA1 MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome, segment 39/162.	Mycobacterium tuberculosis	64,863	17-Jun-98
GB_PAT AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	98,810	05-DEC-1998
EM_PAT E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	98,810	08-OCT-1997 (Rel 52, Created)
GB_PAT E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	98,810	24-Jun-98
GB_PAT E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	99,368	24-Jun-98

Table 4 (continued)

rxa00581	1092	GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	99,368	05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	99,368	08-OCT-1997 (Rel. 52, Created) 24-Jun-98
		GB_PAT:E12594	2104	E12594	DNA encoding serine hydroxymethyltransferase from Brevibacterium flavum.	Corynebacterium glutamicum	37,071	08-OCT-1997 (Rel. 52, Created) 05-DEC-1998
		EM_PAT:E11273	2104	E11273	DNA encoding serine hydroxymethyl transferase.	Corynebacterium glutamicum	37,071	05-DEC-1998
		GB_PAT:AR016483	2104	AR016483	Sequence 1 from patent US 5776740.	Unknown.	37,071	26-Apr-93
rxa00584	1248	GB_BA1:CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,236	29-MAR-1999
		GB_BA1:AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361.	Amycolatopsis orientalis	54,553	7-Feb-99
rxa00618	1230	GB_BA1:D90714	14358	D90714	Escherichia coli genomic DNA (16.8 - 17.1 min).	Escherichia coli	53,312	25-Nov-98
		GB_EST19:AA802737	280	AA802737	GM06236 5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM06236 5prime, mRNA sequence.	Drosophila melanogaster	39,928	18-MAR-1999
		GB_EST28:AI534381	581	AI534381	SD07186 5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD07186 5prime similar to X89858: An F8gn0011558 PID.g927407 SPTREMBL:Q24240, mRNA sequence.	Drosophila melanogaster	41,136	
rxa00619	1551	GB_IN1:DMANILLIN	4029	X89858	D melanogaster mRNA for anillin protein.	Drosophila melanogaster	34,398	8-Nov-95
		GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome, segment 36/162.	Mycobacterium tuberculosis	62,776	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	61,831	24-Jun-97
		GB_PAT:A60305	1845	A60305	Sequence 5 from Patent WO9708323.	unidentified	61,785	06-MAR-1998
rxa00620	1014	GB_PL2:AF063247	1450	AF063247	Pneumocystis carinii f. sp. ratti enolase mRNA, complete cds.	Pneumocystis carinii f. sp. ratti	41,060	5-Jan-99
		GB_BA1:STMAPP	2069	M91546	Streptomyces lividans aminopeptidase P (PepP) gene, complete cds.	Streptomyces lividans	37,126	12-Jun-93
		GB_HTG3:AC008763	214575	AC008763	Homo sapiens chromosome 19 clone CITB-E1_3214H19, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces.	Homo sapiens	40,020	3-Aug-99
rxa00624	810	GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	36,986	2-Sep-99
		GB_EST13:AA362167	372	AA362167	EST71561 Macrophage I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,378	21-Apr-97
		GB_IN1:CEY41E3	150641	Z95559	Caenorhabditis elegans cosmid Y41E3, complete sequence.	Caenorhabditis elegans	37,694	2-Sep-99
rxa00626	1386	GB_BA1:MTCY369	36850	Z80226	Mycobacterium tuberculosis H37Rv complete genome, segment 36/162	Mycobacterium tuberculosis	57,971	17-Jun-98
		GB_BA1:MLCB5	38109	Z95151	Mycobacterium leprae cosmid B5.	Mycobacterium leprae	58,806	24-Jun-97
		GB_BA1:MLU15187	36138	U15187	Mycobacterium leprae cosmid L296.	Mycobacterium leprae	38,007	09-MAR-1995

Table 4 (continued)

rx00632	795	GB_BA1.BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	97,358	3-Feb-99
		GB_PAT.E04041	675	E04041	DNA sequence coding for dethiobiotinsynthetase.	Corynebacterium glutamicum	98,074	29-Sep-97
		GB_PAT.E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	93,814	29-Sep-97
rx00633	1392	GB_BA1.BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds.	Corynebacterium glutamicum	95,690	3-Feb-99
		GB_PAT.E04040	1272	E04040	DNA sequence coding for diamino pelargonic acid aminotransferase.	Corynebacterium glutamicum	95,755	29-Sep-97
		GB_BA2.EHU38519	1290	U38519	Erwinia herbicola adenosylmethionine-8-amino-7-oxononanoate transaminase (bioA) gene, complete cds.	Erwinia herbicola	55,564	4-Nov-96
rx00688	666	GB_BA1.MTV041	28826	AL021958	Mycobacterium tuberculosis H37Rv complete genome; segment 35/162.	Mycobacterium tuberculosis	60,030	17-Jun-98
		GB_BA1.BRLSECY	1516	D14162	Brevibacterium flavum gene for SecY protein (complete cds) and gene or adenylate kinase (partial cds).	Corynebacterium glutamicum	99,563	3-Feb-99
		GB_BA2.MBU77912	7163	U77912	Mycobacterium bovis MBE50a gene, partial cds; and MBE50b, MBE50c, preprotein translocase SecY subunit (secY), adenylate kinase (adk), methionine aminopeptidase (map), RNA polymerase ECF sigma factor (sigE50), MBE50d, and MBE50e genes, complete cds.	Mycobacterium bovis	60,030	27-Jan-99
rx00708	930	GB_BA2.AF157493	25454	AF157493	Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.	Zymomonas mobilis	39,116	5-Jul-99
		GB_PAT.100836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	47,419	21-MAY-1993
		GB_PAT.E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase	unidentified	47,419	29-Sep-97
rx00717	1083	GB_PAT.178753	1187	I78753	Sequence 9 from patent US 5693781.	Unknown.	37,814	3-Apr-98
		GB_PAT.192042	1187	I92042	Sequence 9 from patent US 5726299.	Unknown.	37,814	01-DEC-1998
		GB_BA1.MTC1125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	50,647	17-Jun-98
rx00718	831	GB_BA1.MTC1125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	55,228	17-Jun-98
		GB_BA1.MTC1125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	40,300	17-Jun-98
		GB_GSS12.AQ42075	671	AQ420755	RPCL11-168G18.TJ RPCL11 Homo sapiens genomic clone RPCL11-168G18, genomic survey sequence.	Homo sapiens	35,750	23-MAR-1999
rx00727	1035	GB_HTG3.AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCL1-98 48 D.10 map 34A-34A strain y; cn bw sp. *** SEQUENCING IN PROGRESS	Drosophila melanogaster	40,634	6-Aug-99
		GB_HTG3.AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPCL1-98 48 D.10 map 34A-34A strain y; cn bw sp. *** SEQUENCING IN PROGRESS***, 78 unordered pieces.	Drosophila melanogaster	40,634	6-Aug-99

Table 4 (continued)

rx00766	966	GB_HTG3.AC008332	118545	AC008332	Drosophila melanogaster chromosome 2 clone BACR48D10 (D867) RPC1-98 48.D.10 map 34A-34A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	33,888	6-Aug-99
		GB_HTG2.AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 unordered pieces.	Caenorhabditis elegans	36,737	25-Feb-99
		GB_HTG2.AC006789	83823	AC006789	Caenorhabditis elegans clone Y49F6, *** SEQUENCING IN PROGRESS ***; 2 unordered pieces.	Caenorhabditis elegans	36,737	25-Feb-99
		GB_BA1.D90810	20476	D90810	E. coli genomic DNA, Kohara clone #319(37.4-37.8 min.).	Escherichia coli	36,526	29-MAY-1997
rx00770	1293	GB_BA1.MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome, segment 40/162.	Mycobacterium tuberculosis	66,193	24-Jun-99
		GB_BA1.MLU15182	40123	U15182	Mycobacterium leprae cosmid B2266.	Mycobacterium leprae	61,443	09-MAR-1995
		GB_BA2.SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor A3(2)	59,938	21-Sep-99
rx00779	1056	GB_HTG1.CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_HTG1.CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	64,896	14-OCT-1998
		GB_PL2.AF078693	1492	AF078693	Chlamydomonas reinhardtii putative O-acetylserine(thiol)lyase precursor (Crcys-1A) mRNA, nuclear gene encoding organellar protein, complete cds.	Chlamydomonas reinhardtii	57,970	3-Nov-99
rx00780	669	GB_BA1.MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162.	Mycobacterium tuberculosis	54,410	17-Jun-98
		GB_BA1.AVINIFREG	7099	M60090	Azotobacter chroococcum nitU, nitS, nitP, nitV, nitW, nitZ and nitM genes, complete cds.	Azotobacter chroococcum	51,729	26-Apr-93
		GB_BA2.AF001780	6701	AF001780	Cyanothece PCC 8801 NitP (nitP), nitrogenase (nitB), FdxN (fdxN), NitS (nitS) and NitU (nitU) genes, complete cds, and NitH (nitH) gene, partial cds.	Cyanothece PCC8801	36,309	08-MAR-1999
rx00838	1023	GB_EST1.Z30506	329	Z30506	ATT52430 AC16H Arabidopsis thaliana cDNA clone TAI306 3', mRNA sequence.	Arabidopsis thaliana	44,308	11-MAR-1994
		GB_PL2.AC006258	110469	AC006258	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence.	Arabidopsis thaliana	35,571	28-DEC-1998
		GB_EST37.A1998439	455	A1998439	701545695 A. thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545695, mRNA sequence.	Arabidopsis thaliana	36,044	8-Sep-99
rx00863	867	GB_BA1.BLDAPAB	3572	Z21502	B lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,539	16-Aug-93
		GB_PAT.E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS).	Corynebacterium glutamicum	99,539	28-Jul-99
		GB_PAT.E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	99,539	28-Jul-99
rx00864	873	GB_BA1.BLDAPAB	3572	Z21502	B lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	99,885	16-Aug-93
		GB_BA1.CGDAAPB	1902	X67737	C glutamicum dapB gene for dihydrodipicolinate reductase	Corynebacterium glutamicum	100,000	1-Apr-93

Table 4 (continued)

rx00865	1026	GB_PAT E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase.	Corynebacterium glutamicum	100,000	28-Jul-99
		GB_BA1 BLDAPAB	3572	Z21502	B lactofermentum dapA and dapB genes for dihydrodipicolinate synthase and dihydrodipicolinate reductase.	Corynebacterium glutamicum	100,000	16-Aug-93
		GB_PAT E16752	1411	E16752	gDNA encoding dihydrodipicolinate reductase (DDPR).	Corynebacterium glutamicum	99,805	28-Jul-99
rx00867	650	GB_PAT AR038113	1411	AR038113	Sequence 18 from patent US 5804414.	Unknown.	99,805	29-Sep-99
		GB_BA1 MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	39,179	17-Jun-98
		GB_BA1 MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	39,482	22-Aug-97
		GB_BA1 SAU19858	2838	U19858	Streptomyces antibioticus guanosine pentaphosphate synthetase (gpsI) gene, complete cds.	Streptomyces antibioticus	69,706	25-OCT-1996
rx00873	779	GB_BA1 SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	63,415	29-MAR-1999
		GB_BA1 SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	61,617	29-MAR-1999
rx00884	1263	GB_BA1 D78198	2304	D78198	Pimelobacter sp. DNA for trehalose synthase, complete cds	Pimelobacter sp.	60,594	5-Feb-99
		GB_BA1 MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	37,785	17-Jun-98
		GB_BA1 MSGY222	41156	AD000010	Mycobacterium tuberculosis sequence from clone y222.	Mycobacterium tuberculosis	38,006	03-DEC-1996
		GB_GSS15 AQ65460	468	AQ654600	Sheared DNA-1014 TF Sheared DNA Trypanosoma brucei genomic clone	Trypanosoma brucei	33,974	22-Jun-99
rx00891	1102	GB_BA1 MTCI418B	11700	Z96071	Sheared DNA-1014, genomic survey sequence.	Mycobacterium tuberculosis	63,297	18-Jun-98
		GB_BA1 SCO001206	9184	AJ001206	Mycobacterium tuberculosis H37Rv complete genome; segment 7/162.	Mycobacterium tuberculosis	61,965	29-MAR-1999
		GB_BA1 SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	61,727	29-MAR-1999
rx00952	963	EM_PAT E10963	3118	E10963	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	99,688	08-OCT-1997 (Rel
					gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	52, Created)	10-Feb-99
		GB_BA1 BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,847	29-Sep-97
rx00954	644	GB_PAT E01688	7725	E01688	Genomic DNA of trp operon of preipbacterium latopheimtamn.	unidentified	98,428	29-Sep-97
		GB_PAT E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,758	29-Sep-97
		GB_PAT E01688	7725	E01688	Genomic DNA of trp operon of preipbacterium latopheimtamn.	unidentified	98,758	29-Sep-97
		GB_BA1 BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,758	10-Feb-99
rx00955	1545	GB_PAT E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,372	29-Sep-97

Table 4 (continued)

rx000956	1237	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,372	10-Feb-99
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	unidentified	98,242	29-Sep-97
		EM_PAT:E10963	3118	E10963	gDNA encoding tryptophan synthase.	Corynebacterium glutamicum	98,949	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,107	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,945	29-Sep-97
rx000957	1677	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	99,165	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,927	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	unidentified	98,867	29-Sep-97
rx000958	747	GB_BA1:BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon.	Corynebacterium glutamicum	98,792	10-Feb-99
		GB_PAT:E01375	7726	E01375	DNA sequence of tryptophan operon.	Corynebacterium glutamicum	98,792	29-Sep-97
		GB_PAT:E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentam.	unidentified	98,658	29-Sep-97
rx000970	1050	GB_BA1:CGHOMTHR	3685	Y00546	Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase.	Corynebacterium glutamicum	99,905	12-Sep-93
		GB_PAT:109077	3685	109077	Sequence 1 from Patent WO 8809819.	Unknown.	99,810	02-DEC-1994
		GB_PAT:E01358	2615	E01358	DNA encoding for homoserine dehydrogenase(HDH)and homoserine kinase(HK).	Corynebacterium glutamicum	97,524	29-Sep-97
rx000972	1458	GB_PAT:E16755	3579	E16755	gDNA encoding diaminopimelate decarboxylase (DDC) and arginyl-IRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
		GB_PAT:AR038110	3579	AR038110	Sequence 15 from patent US 5804414.	Unknown.	99,931	29-Sep-99
		GB_PAT:E14508	3579	E14508	DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-IRNA synthase.	Corynebacterium glutamicum	99,931	28-Jul-99
rx000981	753	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	Gallus gallus	37,538	28-Sep-99
		GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F1504 from chromosome I, complete sequence.	Arabidopsis thaliana	37,600	04-OCT-1999
		GB_GSS1:CNS00RN	542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	41,264	28-Jun-99
rx000989	1644	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/162.	Mycobacterium tuberculosis	40,773	17-Jun-98
		GB_BA1:SCVALSFP	3619	Y13070	S.coelicolor valS, fpgs, ndk genes.	Streptomyces coelicolor	58,119	03-MAR-1998
		GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/162	Mycobacterium tuberculosis	38,167	17-Jun-98

Table 4 (continued)

αa00997	705	GB_BA2.CGU31225	1817	U31225	Corynebacterium glutamicum L-proline NADP+ 5-oxido-reductase (proC) gene, Corynebacterium complete cds.	40,841	2-Aug-96
		GB_HTG1.CEY39C12	282838	AL009026	Caenorhabditis elegans chromosome IV clone Y39C12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	36,416	26-OCT-1999
		GB_IN1.CEB0001	39416	Z69634	Caenorhabditis elegans cosmid B0001, complete sequence.	36,416	2-Sep-99
αa01019	1110	GB_HTG2.AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	39,172	12-Jun-98
		GB_HTG2.AC005052	144734	AC005052	Homo sapiens clone RG038K21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	39,172	12-Jun-98
		GB_GSS9.AQ171808	512	AQ171808	Homo sapiens genomic clone Plate=3179 Col=5 Row=M, genomic survey sequence.	34,661	17-OCT-1998
αa01026	1782	GB_BA1.SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	68,275	15-Jan-99
		GB_BA1.ATLEUCD	2982	X84647	A teichomyceticus leuC and leuD genes	65,935	04-OCT-1995
		GB_BA1.MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome, segment 132/162.	40,454	23-Jun-99
αa01027	1131	GB_BA1.MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	38,636	17-Sep-97
		GB_BA1.MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome, segment 131/162.	51,989	17-Jun-98
		GB_BA1.SPUNGMUT X	1172	ZZ1702	S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase.	38,088	15-Jun-94
αa01073	954	GB_BA1.BACOUTB	1004	M15811	Bacillus subtilis outB gene encoding a sporulation protein, complete cds.	53,723	26-Apr-93
		GB_PR4.AC007938	167237	AC007938	Homo sapiens clone UWGC-djs201 from 7q31, complete sequence.	34,322	1-Jul-99
		GB_PL2.ATAC006282	92577	AC006282	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence.	36,181	13-MAR-1999
αa01079	2226	GB_BA2.AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	99,820	5-Aug-99
		GB_BA1.CANRDFGE N	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	75,966	18-Apr-98
		GB_BA1.MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome, segment 132/162.	38,296	23-Jun-99
αa01080	567	GB_BA2.AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	100,000	5-Aug-99
		GB_BA1.CANRDFGE N	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	65,511	18-Apr-98
		GB_BA1.STNRD	4894	X73226	S.typhimurium nrdEF operon.	52,477	03-MAR-1997
αa01087	999	GB_IN2.AF063412	1093	AF063412	Limnadia lenticularis elongation factor 1-alpha mRNA, partial cds.	43,750	29-MAR-1999
		GB_PR3.HS24M15	134539	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restictin). EST.	37,475	23-Nov-99
		GB_IN2.ARU85702	1240	U85702	Anathix ralla elongation factor-1 alpha (EF-1a) gene, partial cds.	37,319	16-Jul-97

Table 4 (continued)

rx01095	857	GB_BA1.MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	43,243	17-Jun-98
		GB_HTG5.AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,471	19-Nov-99
		GB_HTG6.AC011632	175917	AC011632	Homo sapiens clone RP11-3N13, WORKING DRAFT SEQUENCE, 9 unordered pieces.	Homo sapiens	36,836	19-Nov-99
rx01097	477	GB_BA2.AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	100,000	13-Nov-97
		GB_BA2.AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	41,206	13-Nov-97
rx01098	897	GB_BA2.AF030405	774	AF030405	Corynebacterium glutamicum cyclase (hisF) gene, complete cds.	Corynebacterium glutamicum	97,933	13-Nov-97
		GB_BA1.MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	40,972	10-DEC-1996
rx01100	861	GB_BA1.MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	61,366	27-Aug-99
		GB_BA2.AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	97,154	12-MAR-1998
		GB_BA2.AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	95,455	29-Apr-98
rx01101	756	GB_HTG1.HSDJ140A	221755	AL109917	Homo sapiens chromosome 1 clone RP1-140A9, ** SEQUENCING IN PROGRESS **, in unordered pieces.	Homo sapiens	30,523	23-Nov-99
		GB_BA2.AF060558	636	AF060558	Corynebacterium glutamicum glutamine amidotransferase (hisH) gene, complete cds.	Corynebacterium glutamicum	94,462	29-Apr-98
		GB_BA1.SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	38,378	23-Jul-99
rx01104	729	GB_BA1.STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	60,053	26-Apr-93
		GB_BA1.STMHISOPA	3981	M31628	S.coelicolor histidine biosynthesis operon encoding hisD, partial cds., and hisC, hisB, hisH, and hisA genes, complete cds.	Streptomyces coelicolor	58,333	26-Apr-93
		GB_BA1.SC4G6	36917	AL096884	Streptomyces coelicolor cosmid 4G6.	Streptomyces coelicolor A3(2)	39,045	23-Jul-99
rx01105	1221	GB_BA1.MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162	Mycobacterium tuberculosis	60,364	24-Jun-99
		GB_BA1.MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162	Mycobacterium tuberculosis	60,931	24-Jun-99
		GB_BA1.MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	36,851	10-DEC-1996
rx01106	1449	GB_BA1.MLCB1610	40055	AL049913	Mycobacterium leprae cosmid B1610.	Mycobacterium leprae	60,902	27-Aug-99
		GB_BA1.MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,233	10-DEC-1996

Table 4 (continued)

[illegible]

Table 4 (continued)

rx01321	1044	GB_GSS14.AQ51884	441	AQ518843	HS_5106_A1_D10_SPEE RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=682 Col=19 Row=G, genomic survey sequence.	Homo sapiens	41,121	05-MAY-1999
		GB_HTG2.AC007473	194859	AC007473	Drosophila melanogaster chromosome 2 clone BACR38D12 (D590) RPCI-98 38.D.12 map 48A-48B strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	40,634	2-Aug-99
		GB_HTG4.AC011696	115847	AC011696	***, 60 unordered pieces. Drosophila melanogaster chromosome 2 clone BACR35F01 (D1156) RPCI-98 35.F.1 map 48A-48C strain y; cn bw sp, *** SEQUENCING IN PROGRESS	Drosophila melanogaster	38,290	26-OCT-1999
rx01352	706	GB_PL2.ATAC005167	83260	AC005167	***, 108 unordered pieces. Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	15-OCT-1998
		GB_PL2.ATAC005825	97380	AC005825	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.	Arabidopsis thaliana	34,311	12-Apr-99
		GB_HTG3.AC011150	127222	AC011150	Homo sapiens clone 4_K_17, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	37,722	01-OCT-1999
rx01360	259	GB_EST32.A1725583	728	A1725583	BNLGH12371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U86081) root hair defective 3 [Arabidopsis thaliana], mRNA sequence. Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.	Gossypium hirsutum	38,492	11-Jun-99
		GB_PR2.HS227P17	82951	Z81007	AV171099 Mus musculus head C57BL/6J 14, 17 day embryo Mus musculus cDNA clone 3200002M11, mRNA sequence.	Mus musculus	46,237	6-Jul-99
rx01361	629	GB_RO.AB008915S1	530	AB008915	Mus musculus mGp11 gene, exon 1.	Mus musculus	45,574	28-Sep-99
		GB_EST22.A1050532	293	A1050532	uc83d10.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:1432243 5' similar to TR:O35120 O35120 MGPI1P.1, mRNA sequence.	Mus musculus	44,097	9-Jul-98
rx01381	944	GB_RO.AB008895	3062	AB008895	Mus musculus mRNA for mGp11p, complete cds.	Mus musculus	41,316	23-Nov-97
		GB_PL1.AB005237	87835	AB005237	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence.	Arabidopsis thaliana	36,606	20-Nov-99
		GB_GSS5.AQ766840	491	AQ766840	HS_2026_A2_C09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=18 Row=E, genomic survey sequence.	Homo sapiens	37,916	28-Jul-99
		GB_BA1.MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome, segment 40/162.	Mycobacterium tuberculosis	37,419	24-Jun-99
rx01393	993	GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.	Corynebacterium glutamicum	34,831	24-Feb-97
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7	Streptomyces coelicolor	35,138	27-Jul-98
		GB_PR3.AC004054	112184	AC004054	Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.	Homo sapiens	37,277	9-Jul-98
rx01394	822	GB_BA1:CGLYSEG	2374	X96471	C. glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
		GB_GSS5.AQ769223	500	AQ769223	HS_3155_B2_G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=20 Row=N, genomic survey sequence.	Homo sapiens	38,400	28-Jul-99

*glutamicum lysE* and *lysG* genes.

[illegible]

Table 4 (continued)

rx01514	711	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	40,086	17-Jun-98
		GB_BA1:MTY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	43,343	18-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	38,177	27-Aug-99
		GB_PL1:EGGTPCHI	242	Z49757	E. gracilis mRNA for GTP cyclohydrolase I (core region).	Euglena gracilis	64,876	20-OCT-1995
rx01515	975	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,943	17-Apr-96
		GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,500	17-Apr-96
		GB_BA1:MTY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	38,010	24-Jun-99
rx01516	513	GB_IN1:DME238847	5419	AJ238847	Drosophila melanogaster mRNA for drosophila dodeca-satellite protein 1 (DDP-1).	Drosophila melanogaster	36,346	13-Aug-99
		GB_HTG3:AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01106 (D1054) RPCI-98 01.1.6 map 55D strain y; cn bw sp. *** SEQUENCING IN PROGRESS	Drosophila melanogaster	37,897	20-Aug-99
rx01517	600	GB_IN2:AF132179	4842	AF132179	***, 86 unordered pieces.	Drosophila melanogaster	36,149	3-Jun-99
		GB_PL2:F6H8	82596	AF178045	Drosophila melanogaster clone LD21677 unknown mRNA.	Arabidopsis thaliana	35,846	19-Aug-99
		GB_PL2:AF038831	647	AF038831	Sorosporium saponariae internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.	Sorosporium saponariae	40,566	13-Apr-99
		GB_PL2:ATAC005957	108355	AC005957	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence.	Arabidopsis thaliana	38,095	7-Jan-99
rx01521	921	GB_BA1:ANANIFBH	5936	J05111	Anabaena sp. (clone AnH20.1) nitrogen fixation operon nifB, fdxN, nifS, nifU, and nifH genes, complete cds.	Anabaena sp.	38,206	26-Apr-93
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from 7q31, complete sequence.	Homo sapiens	36,623	20-Aug-97
		GB_PR2:AC002461	197273	AC002461	Human BAC clone RG204116 from 7q31, complete sequence.	Homo sapiens	34,719	20-Aug-97
		GB_RO:MM437P9	165901	AL049866	Mus musculus chromosome X, clone 437P9.	Mus musculus	37,500	29-Jun-99
rx01528	651	GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	37,031	01-OCT-1998
		GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.	Homo sapiens	38,035	01-OCT-1998
rx01551	1998	GB_BA1:MTY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	38,371	17-Jun-98
		GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	38,064	17-DEC-1993
rx01561	1053	GB_BA1:SCQ11	15441	AL096823	Streptomyces coelicolor cosmid Q11	Streptomyces coelicolor	60,775	8-Jul-99
		GB_IN1:CEY62H9A	47396	AL032630	Caenorhabditis elegans cosmid Y62H9A, complete sequence.	Caenorhabditis elegans	38,514	2-Sep-99
		GB_PR4:HSU51003	3202	U51003	Homo sapiens DLX-2 (DLX-2) gene, complete cds.	Homo sapiens	37,730	07-DEC-1999
rx01599	1785	GB_OM:PIGDAO1	395	M18444	Pig D-amino acid oxidase (DAO) gene, exon 1.	Sus scrofa	39,340	27-Apr-93
		GB_BA1:MTCT125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome; segment 76/162.	Mycobacterium tuberculosis	63,300	17-Jun-98
		GB_BA1:U00021	39193	U00021	Mycobacterium leprae cosmid L247.	Mycobacterium leprae	36,756	29-Sep-94

Table 4 (continued)

αa01617	795	GB_BA1_MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351.	Mycobacterium leprae	36,756	24-Jun-97
		GB_PR2_HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100, complete sequence bases 1..217657.	Homo sapiens	40,811	5-Jul-99
αa01657	723	GB_PR2_HS13D10	153147	AL021407	Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.	Homo sapiens	38,768	23-Nov-99
		GB_PR2_HSMTM0	217657	AL034384	Human chromosome Xq28, cosmid clones 7H3, 14D7, C1230, 11E7, F1096, A12197, 12G8, A09100, complete sequence bases 1..217657.	Homo sapiens	39,018	5-Jul-99
αa01660	675	GB_BA1_MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	40,656	17-Jun-98
		GB_EST6_D79278	392	D79278	HUM213D06B Human aorta polyA+ (TF ujiwara) Homo sapiens cDNA clone GEN-213D06 5' mRNA sequence.	Homo sapiens	44,262	9-Feb-96
αa01660	675	GB_BA2_AF129925	10243	AF129925	Thiobacillus ferrooxidans carboxysome operon, complete cds.	Thiobacillus ferrooxidans	40,709	17-MAY-1999
		GB_BA1_MTV013	11364	AL021309	Mycobacterium tuberculosis H37Rv complete genome; segment 134/162.	Mycobacterium tuberculosis	40,986	17-Jun-98
αa01678	651	GB_RO_MMV1	6480	X97719	M. musculus retrovirus restriction gene Fv1.	Mus musculus	35,364	29-Aug-96
		GB_PAT_A67508	6480	A67508	Sequence 1 from Patent WO9743410.	Mus musculus	35,364	05-MAY-1999
αa01679	1359	GB_VI_TVU95309	600	U95309	Tula virus O64 nucleocapsid protein gene, partial cds.	Tula virus	41,894	28-OCT-1997
		GB_VI_TVU95303	600	U95303	Tula virus O52 nucleocapsid protein gene, partial cds.	Tula virus	41,712	28-OCT-1997
αa01690	1224	GB_VI_TVU95302	600	U95302	Tula virus O24 nucleocapsid protein gene, partial cds.	Tula virus	39,576	28-OCT-1997
		GB_EST5_H91843	362	H91843	ys81e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:221208 3' similar to gb.X63749_rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 (HUMAN); mRNA sequence.	Homo sapiens	39,157	29-Nov-95
αa01692	873	GB_STS_G26925	362	G26925	human STS SHGC-30023, sequence tagged site.	Homo sapiens	39,157	14-Jun-96
		GB_PL2_AF139451	1202	AF139451	Gossypium robinsonii CeiA2 pseudogene, partial sequence.	Gossypium robinsonii	38,910	1-Jun-99
αa01698	1353	GB_BA1_SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	60,644	15-Jan-99
		GB_EST22_A1064232	493	A1064232	GH04563.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH04563 5prime, mRNA sequence.	Drosophila melanogaster	38,037	24-Nov-98
αa01692	873	GB_IN2_AF117896	1020	AF117896	Drosophila melanogaster neurotrophin F (npf) gene, complete cds.	Drosophila melanogaster	36,122	2-Jul-99
		GB_BA2_AF067123	1034	AF067123	Lactobacillus reuteri cobalamin biosynthesis protein J (cbiJ) gene, partial cds. and uroporphyrin-III C-methyltransferase (sumT) gene, complete cds.	Lactobacillus reuteri	48,079	3-Jun-98
αa01698	1353	GB_RO_RATNFHPEP	3085	M37227	Rat heavy neurofilament (NF-H) polypeptide, partial cds.	Rattus norvegicus	37,093	27-Apr-93
		GB_RO_RSNFH	3085	X13804	Rat mRNA for heavy neurofilament polypeptide NF-H C-terminus.	Rattus sp	37,093	14-Jul-95
αa01698	1353	GB_BA2_AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds; and putative cytoplasmic peptidase (pepQ) gene, partial cds.	Corynebacterium glutamicum	100,000	04-MAY-1999
		GB_BA1_MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	36,323	17-Jun-98



Table 4 (continued)

rx01807	915	GB_BA1:AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7.	Aeropyrum pernix	40,067	22-Jun-99
		GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	Drosophila melanogaster	35,450	16-OCT-1999
		GB_HTG4:AC010694	115857	AC010694	Drosophila melanogaster clone RPC198-6H2, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.	Drosophila melanogaster	35,450	16-OCT-1999
rx01821	401	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_RO:RATALGL	7601	M24108	Rattus norvegicus (clone A2U42) alpha2u globulin gene, exons 1-7.	Rattus norvegicus	38,692	15-DEC-1994
rx01835	654	GB_OV:APIGY2	1381	X78272	Anas platyrhynchos (Super M) IgY upslon heavy chain gene, exon 2	Anas platyrhynchos	36,962	15-Feb-99
		GB_EST30:AI629479	353	AI629479	486101D10.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.	Zea mays	38,109	26-Apr-99
		GB_STS:G48245	515	G48245	SHGC-62915 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	37,021	26-MAR-1999
rx01850	1470	GB_GSS3:B49052	515	B49052	RPC11-4112 TV RPC1-11 Homo sapiens genomic clone RPC1-11-4112, genomic survey sequence.	Homo sapiens	37,021	8-Apr-99
		GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,196	U18997
rx01878	1002	GB_HTG1:CEY64F11	177748	Z99776	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome.	Escherichia coli	38,021	12-Nov-98
		GB_HTG1:CEY64F11	177748	Z99776	Haemophilus influenzae Rd section 30 of 163 of the complete genome.	Haemophilus influenzae Rd	39,860	29-MAY-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,564	14-OCT-1998
		GB_HTG1:CEY64F11	177748	Z99776	Caenorhabditis elegans chromosome IV clone Y64F11, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	37,576	14-OCT-1998
rx01892	852	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	35,910	19-Jun-98
		GB_BA1:MLCB250	40603	Z97369	Mycobacterium leprae cosmid B250.	Mycobacterium leprae	64,260	27-Aug-99
		GB_BA1:MSG1529C	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	Mycobacterium leprae	64,260	15-Jun-96
rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPC1-98 03 E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rx01920	1125	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	Corynebacterium glutamicum	99,733	5-Aug-99
		GB_BA1:CANRDFGE	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	70,321	18-Apr-98

Table 4 (continued)

Table 4 (Continued)								
rx01928	960	GB_BA2:AF050168	1228	AF050168	Corynebacterium ammoniagenes ribonucleoside diphosphate reductase small subunit (nrdF) gene, complete cds.	Corynebacterium ammoniagenes	72,082	
		GB_BA1:CGPAN	2164	X96580	C glutamicum panB, panC & xylB genes	Corynebacterium glutamicum	100,000	
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	35,917	
		GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	33,925	
		GB_BA1:CGPAN	2164	X96580	C glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	100,000	
rx01929	936	GB_BA1:XCU33548	8429	U33548	Xanthomonas campestris hrpB pathogenicity locus proteins HrpB1, HrpB2, HrpB3, HrpB4, HrpB5, HrpB6, HrpB7, HrpB8, HrpA1, and ORF62 genes, complete cds.	Xanthomonas campestris pv. vesicatoria	38,749	
		GB_BA1:XANHRPB6A	1329	M99174	Xanthomonas campestris hrpB6 gene, complete cds.	Xanthomonas campestris	39,305	
	rx01940	1059	GB_IN2:CFHJ03371	1060	U43371	Crithidia fasciculata inosine-uridine preferring nucleoside hydrolase (IUNH) gene, complete cds.	Crithidia fasciculata	61,417
			GB_BA2:AF001467	11601	AE001467	Helicobacter pylori, strain J99 section 28 of 132 of the complete genome.	Helicobacter pylori J99	38,560
			GB_ROA1:J5967	3492	AF175967	Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds	Mus musculus	40,275
rx02022	1230	GB_BA1:CGDAPE	1966	X81379	C glutamicum dapE gene and orf2.	Corynebacterium glutamicum	100,000	
		GB_BA1:CGDNAARO P	2612	X85965	C glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	38,889	
		GB_BA1:APU47055	6469	U47055	Anabaena PCC7120 nitrogen fixation proteins (nifE, nifN, nifX, nifW) genes, complete cds, and nitrogenase (nifK) and hesA genes, partial cds.	Anabaena PCC7120	36,647	
	rx02024	859	GB_BA1:MTIC364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome, segment 52/162	Mycobacterium tuberculosis	59,415
			GB_BA1:MSGB1912C S	38503	L01536	M. leprae genomic dna sequence, cosmid b1912.	Mycobacterium leprae	57,093
rx02027		GB_BA1:MLU15180	38675	U15180	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	57,210	
	rx02031							
	rx02072	1464	GB_BA1:CGGDHA	2037	X72855	C glutamicum GDHA gene.	Corynebacterium glutamicum	99,317
		GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	94,387	
		GB_BA1:PAE18494	1628	Y18494	Pseudomonas aeruginosa gdhA gene, strain PAC1.	Pseudomonas aeruginosa	62,247	
rx02079								

Table 4 (continued)

αa02085	2358	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,442	17-Jun-98
		GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	56,486	24-Jun-97
		GB_BA1:ECOUW85	91414	M87049	E. coli genomic sequence of the region from 84.5 to 86.5 minutes.	Escherichia coli	52,127	29-MAY-1995
αa02093	927	GB_EST14:AA448146	452	AA448146	zw82h01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782737	Homo sapiens	34,163	4-Jun-97
		GB_EST17:AA641937	444	AA641937	5', mRNA sequence.			
		GB_PR3:AC003074	143029	AC003074	ns18b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1183963	Homo sapiens	35,586	27-OCT-1997
		GB_BA1:SC1A6	37620	AL023496	5', mRNA sequence.			
αa02106	1179	GB_PR4:AC005553	179651	AC005553	Human PAC clone DJ059009 from 7p15, complete sequence.	Homo sapiens	31,917	6-Nov-97
		GB_EST3:R49746	397	R49746	Streptomyces coelicolor cosmid 1A6.	Streptomyces coelicolor	35,818	13-Jan-99
		GB_BA1:SC6G10	36734	AL049497	Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.	Homo sapiens	34,274	31-DEC-1998
αa02111	1407	GB_BA1:U00010	41171	U00010	yg71g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38768 5' similar to gb.V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN); mRNA sequence.	Homo sapiens	41,162	18-MAY-1995
		GB_BA1:MTCY336	32437	Z95586	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
αa02112	960	GB_HTG3:AC010579	157658	AC010579	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
		GB_GSS3:B09839	1191	B09839	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
		GB_HTG3:AC010579	157658	AC010579	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 Drosophila melanogaster		37,909	24-Sep-99
		GB_GSS3:B09839	1191	B09839	09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS			
		GB_HTG3:AC010579	157658	AC010579	***, 121 unordered pieces.			
		GB_BA1:SCSECYDN	6154	X83011	T12A12-Sp6 TAMU Arabidopsis thaliana genomic clone T12A12, genomic survey sequence.	Arabidopsis thaliana	37,843	14-MAY-1997
αa02134	1044	GB_BA1:SCSECYDN	6154	X83011	Drosophila melanogaster chromosome 3 clone BACR09D08 (D1101) RPCI-98 Drosophila melanogaster		37,909	24-Sep-99
		GB_EST32:AI731596	568	AI731596	09.D.8 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS			
		GB_BA1:SCSECYDN	6154	X83011	***, 121 unordered pieces.			
		GB_EST32:AI731596	568	AI731596	S. coelicolor secY locus DNA.	Streptomyces coelicolor	36,533	02-MAR-1998
αa02135	1197	GB_PR3:HS25L6	168111	AL023807	BNLGH10185 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004005) putative ribosomal protein L7 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	33,451	11-Jun-99
		GB_PL2:ATF2IP8	85785	AL022347	S. coelicolor secY locus DNA.	Streptomyces coelicolor	36,756	02-MAR-1998
		GB_PL2:ATF2IP8	85785	AL022347	Human DNA sequence from clone RP3.525L6 on chromosome 6p22.3-23 Contains CA repeat, STSs, GSSs and a CpG Island, complete sequence.	Homo sapiens	34,365	23-Nov-99
		GB_PL2:ATF2IP8	85785	AL022347	Arabidopsis thaliana DNA chromosome 4, BAC clone F21P8 (ESSA project).	Arabidopsis thaliana	34,325	9-Jun-99
		GB_PL2:U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	33,874	26-Jun-98

Table 4 (continued)

rx02136	645	GB_PL2.ATAC005819	57752	AC005819	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence.	Arabidopsis thaliana	34,123	3-Nov-98
		GB_PL2.F15K9	71097	AC005278	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.	Arabidopsis thaliana	31,260	7-Nov-98
		GB_PL2.U89959	106973	U89959	Arabidopsis thaliana BAC T7123, complete sequence.	Arabidopsis thaliana	34,281	26-Jun-98
rx02139	1962	GB_BA1.MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome, segment 98/162.	Mycobacterium tuberculosis	62,904	17-Jun-98
		GB_BA1.MSGB*554C	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
		GB_BA1.MSGB*551C	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	36,648	15-Jun-96
rx02153	903	GB_BA2.AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,104	1-Jul-98
		GB_BA1.AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	99,224	2-Jul-97
		GB_BA1.CGARGCJB	4355	X86157	C glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02154	414	GB_BA2.AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	98,551	1-Jul-98
		GB_BA1.AF005242	1044	AF005242	Corynebacterium glutamicum N-acetylglutamate-5-semialdehyde dehydrogenase (argC) gene, complete cds.	Corynebacterium glutamicum	98,477	2-Jul-97
		GB_BA1.CGARGCJB	4355	X86157	C glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
rx02155	1287	GB_BA1.CGARGCJB	4355	X86157	C glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,767	25-Jul-96
		GB_BA2.AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,378	1-Jul-98
		GB_BA1.MSGB1133C	42106	L78811	Mycobacterium leprae cosmid B1133 DNA sequence.	Mycobacterium leprae	55,504	15-Jun-96
rx02156	1074	GB_BA2.AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98

Table 4 (continued)

GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
D						
GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	50,238	2-Jun-99
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,612	1-Jul-98
GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	99,612	25-Jul-96
D						
GB_BA1:MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome, segment 73/162.	Mycobacterium tuberculosis	57,278	17-Jun-98
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	100,000	1-Jul-98
GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	99,898	5-Jan-99
GB_BA1:CGARGCJB	4355	X86157	C. glutamicum argC, argJ, argB, argD, and argF genes.	Corynebacterium glutamicum	100,000	25-Jul-96
D						
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.	Corynebacterium glutamicum	88,679	5-Jan-99
GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	99,774	1-Jul-98
GB_BA2:AF030520	1206	AF030520	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,834	19-Nov-97
GB_BA1:SCARGGH	1909	Z49111	S. clavuligerus argG gene and argH gene (partial).	Streptomyces clavuligerus	65,913	22-Apr-96
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamate kinase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	88,524	1-Jul-98

Table 4 (continued)

Table 4 (continued)

948	948	GB_PR4:AC006236	127593	AC006236	127593	Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.	Homo sapiens	37,191	29-DEC-1998
948	948	GB_BA1:MSGY154	40221	AD000102	40221	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	53,541	03-DEC-1996
948	948	GB_BA1:MTCY154	13935	Z98209	13935	Mycobacterium tuberculosis H37Rv complete genome; segment 121/162.	Mycobacterium tuberculosis	40,407	17-Jun-98
3462	3462	GB_BA1:U00019	36033	U00019	36033	Mycobacterium leprae cosmid B2235.	Mycobacterium leprae	40,541	01-MAR-1994
3462	3462	GB_BA1:MSGB937C	38914	L78820	38914	Mycobacterium leprae cosmid B937 DNA sequence.	Mycobacterium leprae	66,027	15-Jun-96
727	727	GB_BA1:MTCY2B12	20431	Z81011	20431	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	71,723	18-Jun-98
727	727	GB_BA2:U01072	4393	U01072	4393	Mycobacterium bovis BCG oroidine-5'-monophosphate decarboxylase (uraA) gene.	Mycobacterium bovis	67,101	22-DEC-1993
727	727	GB_BA1:MSU91572	960	U91572	960	Mycobacterium smegmatis carbamoyl phosphate synthetase (pyrAB) gene, partial cds and oroidine 5'-monophosphate decarboxylase (pyrF) gene, complete cds.	Mycobacterium smegmatis	60,870	22-MAR-1997
693	693	GB_HTG3:AC009364	192791	AC009364	192791	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
693	693	GB_HTG3:AC009364	192791	AC009364	192791	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***; 57 unordered pieces.	Homo sapiens	37,994	1-Sep-99
693	693	GB_BA1:MTCY21B4	39150	Z80108	39150	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	55,844	23-Jun-98
1389	1389	GB_BA2:AF077324	5228	AF077324	5228	Rhodococcus equi strain 103 plasmid RE-VP1 fragment f.	Rhodococcus equi	41,185	5-Nov-98
1389	1389	GB_EST22:AU017763	586	AU017763	586	AU017763 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0744A04 3', mRNA sequence.	Mus musculus	38,616	19-OCT-1998
1389	1389	GB_BA1:MTCY21B4	39150	Z80108	39150	Mycobacterium tuberculosis H37Rv complete genome; segment 62/162.	Mycobacterium tuberculosis	56,282	23-Jun-98
1344	1344	GB_HTG3:AC010745	193862	AC010745	193862	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
1344	1344	GB_HTG3:AC010745	193862	AC010745	193862	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***; 30 unordered pieces.	Homo sapiens	36,772	21-Sep-99
1344	1344	EM_PAT:E09855	1239	E09855	1239	gDNA encoding S-adenosylmethionine synthetase.	Corynebacterium glutamicum	99,515	07-OCT-1997 (Rel. 52, Created)
1107	1107	GB_PAT:A37831	5392	A37831	5392	Sequence 1 from Patent WO9408014.	Streptomyces pristinaespiralis	63,568	05-MAR-1997
1107	1107	GB_BA2:AF117274	2303	AF117274	2303	Streptomyces spectabilis flavoprotein homolog Dfp (dfr) gene, partial cds, and Streptomyces spectabilis S-adenosylmethionine synthetase (metK) gene, complete cds.	Streptomyces spectabilis	65,000	31-MAR-1999
1107	1107	EM_BA1:AB003693	5589	AB003693	5589	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	52,909	03-OCT-1997 (Rel. 52, Created)

Table 4 (continued)

rx02247	756	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	52,909	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	52,909	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 5589355.	Unknown.	57,937	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	57,937	03-OCT-1997 (Rel. 52, Created)
rx02248	1389	GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown	57,937	6-Feb-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	61,843	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	61,843	03-OCT-1997 (Rel. 52, Created)
rx02249	600	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	61,843	29-Sep-97
		GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	64,346	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	64,346	6-Feb-97
		GB_PAT:132743	2689	132743	Sequence 2 from patent US 5589355.	Unknown.	64,346	6-Feb-97
rx02250	643	GB_PAT:E07957	5589	E07957	gDNA encoding at least guanosine triphosphate cyclohydrolase and riboflavin synthase.	Corynebacterium ammoniagenes	56,318	29-Sep-97
		GB_PAT:132742	5589	132742	Sequence 1 from patent US 5589355.	Unknown.	56,318	6-Feb-97
		EM_BA1:AB003693	5589	AB003693	Corynebacterium ammoniagenes DNA for rib operon, complete cds.	Corynebacterium ammoniagenes	56,318	03-OCT-1997 (Rel. 52, Created)
rx02262	1269	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGEN E	2028	X93513	C. glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
		GB_VI:HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome.	human herpesvirus 5	38,651	10-Feb-99
rx02263	488	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	37,526	7-Jan-99
rx02272	1368	EM_PAT:E09373	1591	E09373	Creatinine deiminase gene.	Bacillus sp.	96,928	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:D38505	1591	D38505	Bacillus sp. gene for creatinine deaminase, complete cds.	Bacillus sp.	96,781	7-Aug-98
		GB_HTG2:AC006595	146070	AC006595	Homo sapiens, *** SEQUENCING IN PROGRESS ***	Homo sapiens	36,264	20-Feb-99
rx02281	1545	GB_GSS12:AQ41101	551	AQ411010	HS_2257_B1_H02_MR CIT Approved Human Genomic Sperm Library D	Homo sapiens	36,197	17-MAR-1999
		0			Homo sapiens genomic clone Plate=2257 Col=3 Row=P, genomic survey sequence.			

Table 4 (continued)

αa02299	531	GB_EST23:AI128623	363	AI128623	gb62c01.s1 Soares_fetal_heart_Nb-H19W Homo sapiens cDNA clone IMAGE:1691328 3', mRNA sequence.	Homo sapiens	37,017	05-OCT-1998
		GB_PL2.ATAC007019	102335	AC007019	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence.	Arabidopsis thaliana	33,988	16-MAR-1999
		GB_BA2.AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds.	Corynebacterium glutamicum	100,000	02-MAY-1999
		GB_GSS9.AQ164310	507	AQ164310	HS_2171_A2_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=2 Row=1, genomic survey sequence.	Homo sapiens	37,278	16-OCT-1998
		GB_VI.MH68TKH	4557	X93468	Murine herpesvirus type 68 thymidine kinase and glycoprotein H genes.	murine herpesvirus 68	40,288	3-Sep-96
αa02311	813	GB_HTG4.AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 Drosophila map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
		GB_HTG4.AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 Drosophila map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Drosophila melanogaster	36,454	27-OCT-1999
		GB_BA2.RRU65510	16259	U65510	Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooU, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds.	Rhodospirillum rubrum	37,828	9-Apr-97
αa02315	1752	GB_BA1.MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	49,418	03-DEC-1996
		GB_BA1.MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	49,360	17-Jun-98
		GB_BA1.MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	38,150	03-DEC-1996
αa02318	402	GB_HTG3.AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3.AC011348	111083	AC011348	Homo sapiens chromosome 5 clone CIT-HSPC_303E13, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	Homo sapiens	35,821	06-OCT-1999
		GB_HTG3.AC011412	89234	AC011412	Homo sapiens chromosome 5 clone CIT978SKB_81K21, *** SEQUENCING IN PROGRESS ***; 3 ordered pieces.	Homo sapiens	36,181	06-OCT-1999
αa02319	1080	GB_BA1.MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	37,792	03-DEC-1996
		GB_BA1.MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	37,792	17-Jun-98
		GB_EST23.AI117213	476	AI117213	ub83h02.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1395123 5', mRNA sequence.	Mus musculus	35,084	2-Sep-98

Table 4 (continued)

αa02345	1320	GB_BA1:BAPURKE	2582	X91189	B. ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	61,731	14-Jan-97
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,624	10-Feb-99
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,847	10-Feb-99
αa02350	618	GB_BA1:BAPURKE	2582	X91189	B. ammoniagenes purK and purE genes.	Corynebacterium ammoniagenes	64,286	14-Jan-97
		GB_PL1:SC130KBXV	129528	X94335	S. cerevisiae 130kb DNA fragment from chromosome XV.	Saccharomyces cerevisiae	36,617	15-Jul-97
		GB_PL1:SCXVORFS	50984	X90518	S. cerevisiae DNA of 51 Kb from chromosome XV right arm.	Saccharomyces cerevisiae	36,617	1-Nov-95
αa02373	1038	GB_PAT:E00311	1853	E00311	DNA coding of 2,5-diketogluconic acid reductase.	unidentified	56,123	29-Sep-97
		GB_PAT:I06030	1853	I06030	Sequence 4 from Patent EP 0305608.	Unknown.	56,220	02-DEC-1994
		GB_PAT:I00836	1853	I00836	Sequence 1 from Patent US 4758514.	Unknown.	56,220	21-MAY-1993
αa02375	1350	GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	99,332	2-Aug-96
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces	Homo sapiens	36,115	8-Sep-99
		GB_HTG3:AC009946	169072	AC009946	Homo sapiens clone NH0012C17, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces	Homo sapiens	36,115	8-Sep-99
αa02380	777	GB_BA1:MTCY253	41230	Z81368	Mycobacterium tuberculosis H37Rv complete genome; segment 106/162.	Mycobacterium tuberculosis	38,088	17-Jun-98
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L75C1 clone RPCI98-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
		GB_HTG4:AC010658	120754	AC010658	Drosophila melanogaster chromosome 3L75C1 clone RPCI98-3B20, *** SEQUENCING IN PROGRESS ***; 78 unordered pieces.	Drosophila melanogaster	35,817	16-OCT-1999
αa02382	1419	GB_BA1:CGPROAGE	1783	X82929	C. glutamicum proA gene.	Corynebacterium glutamicum	98,802	23-Jan-97
		GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	38,054	17-Jun-98
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Obg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unkdh) gene, complete cds.	Corynebacterium glutamicum	98,529	2-Aug-96
αa02400	693	GB_BA1:CGACEA	2427	X75504	C. glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_PAT:I86191	2135	I86191	Sequence 3 from patent US 5700661.	Unknown.	100,000	10-Jun-98
		GB_PAT:I13693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	100,000	26-Sep-95
αa02432	1098	GB_GSS15:AQ60684	574	AQ60684	HS_5404_B2_E07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=14 Row=J, genomic survey sequence.	Homo sapiens	39,716	10-Jun-99

Table 4 (continued)

Table 4 (continued)

rx02517	570	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162	Mycobacterium tuberculosis	61,335	17-Jun-98
		GB_BA1:MLCL535	36224	Z99125	Mycobacterium leprae cosmid L536	Mycobacterium leprae	37,018	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496	Mycobacterium leprae	37,018	01-MAR-1994
rx02532	1170	GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22	Streptomyces coelicolor	37,071	12-Jul-99
		GB_OV:AF137219	831	AF137219	Amia calva mixed lineage leukemia-like protein (Mli) gene, partial cds.	Amia calva	36,853	7-Sep-99
		GB_EST30:AI645057	301	AI645057	vs52a10.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	41,860	29-Apr-99
		GB_EST20:AA822595	429	AA822595	vs52a10.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1149882 5', mRNA sequence.	Mus musculus	42,353	17-Feb-98
rx02536	879	GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_HTG2:AF130866	118874	AF130866	Homo sapiens chromosome 8 clone PAC 172N13 map 8q24, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	40,754	21-MAR-1999
		GB_PL1:ATT12J5	84499	AL035522	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAll project), Arabidopsis thaliana	Arabidopsis thaliana	35,063	24-Feb-99
rx02550	1434	GB_BA1:MTCY279	9150	Z97991	Mycobacterium tuberculosis H37Rv complete genome; segment 17/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
		GB_BA1:MSG81970C	39399	L78815	Mycobacterium leprae cosmid B1970 DNA sequence.	Mycobacterium leprae	39,024	15-Jun-96
		GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	37,906	19-OCT-1999
rx02559	1026	GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	47,358	18-Jun-98
		GB_PAT1:28684	5100	I28684	Sequence 1 from patent US 5573915.	Unknown	39,138	6-Feb-97
		GB_BA1:MTU27357	5100	U27357	Mycobacterium tuberculosis cyclopropane mycolic acid synthase (cma1) gene, complete cds.	Mycobacterium tuberculosis	39,138	26-Sep-95
rx02622	1683	GB_BA2:AE001780	11997	AE001780	Thermotoga maritima section 92 of 136 of the complete genome.	Thermotoga maritima	44,914	2-Jun-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	39,732	17-Aug-99
		GB_OV:AF064564	49254	AF064564	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds.	Fugu rubripes	36,703	17-Aug-99
rx02623	714	GB_GSS5:AQ818728	444	AQ818728	HS_5268_A1_G09_SP6E RPCL1-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=17 Row=M, genomic survey sequence.	Homo sapiens	38,801	26-Aug-99
		GB_HTG5:AC011083	198586	AC011083	Homo sapiens chromosome 9 clone RP11-111M7 map 9, WORKING DRAFT SEQUENCE, 51 unordered pieces.	Homo sapiens	35,714	19-Nov-99
		GB_GSS6:AQ826948	544	AQ826948	HS_5014_A2_C12_T7A RPCL1-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=24 Row=E, genomic survey sequence.	Homo sapiens	39,146	27-Aug-99

Table 4 (continued)

αa02629	708	GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	28-Apr-93
		GB_VI:BRSMGP	462	M86652	Bovine respiratory syncytial virus membrane glycoprotein mRNA, complete cds.	Bovine respiratory syncytial virus	28-Apr-93
αa02645	1953	GB_PAT:A45577	1925	A45577	Sequence 1 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45581	1925	A45581	Sequence 5 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
αa02646	1392	GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (livA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_BA1:CORILVA	1925	L01508	Corynebacterium glutamicum threonine dehydratase (livA) gene, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:A45585	1925	A45585	Sequence 9 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
		GB_PAT:A45583	1925	A45583	Sequence 7 from Patent WO9519442.	Corynebacterium glutamicum	07-MAR-1997
αa02648	1326	GB_OV:ICTCNC	2049	M83111	Ictalurus punctatus cyclic nucleotide-gated channel RNA sequence.	Ictalurus punctatus	24-MAY-1993
		GB_EST11:AA265464	345	AA265464	mx91c06.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:693706 5' mRNA sequence.	Mus musculus	20-MAR-1997
αa02653		GB_GSS8:AQ006950	480	AQ006950	CIT-HSP-2294E14, TR CIT-HSP Homo sapiens genomic clone 2294E14, genomic survey sequence.	Homo sapiens	27-Jun-98
αa02687	1068	GB_BA1:CORPHEA	1088	M13774	C. glutamicum pheA gene encoding prephenate dehydratase, complete cds.	Corynebacterium glutamicum	26-Apr-93
		GB_PAT:E04483	948	E04483	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
		GB_PAT:E06110	948	E06110	DNA encoding prephenate dehydratase.	Corynebacterium glutamicum	29-Sep-97
αa02717	1005	GB_PL1:HVCH4H	59748	Y14573	Hordeum vulgare DNA for chromosome 4H.	Hordeum vulgare	25-MAR-1999
		GB_PR2:HS310H5	29718	Z69705	Human DNA sequence from cosmid 310H5 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains EST and CpG island.	Homo sapiens	22-Nov-99
		GB_PR3:AC004754	39188	AC004754	Homo sapiens chromosome 16, cosmid clone RT286 (LANL), complete sequence.	Homo sapiens	28-MAY-1998
αa02754	1461	GB_HTG2:AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPC1-98 16.1.18 map 95A-95A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	2-Aug-99

Table 4 (continued)

GB_HTG2 AC008223	130212	AC008223	Drosophila melanogaster chromosome 3 clone BACR16118 (D815) RPCI-98 16.118 map 95A-95A strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** 101 unordered pieces.	Drosophila melanogaster	32,757	2-Aug-99
GB_BA1.MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome, segment 141/162.	Mycobacterium tuberculosis	37,838	10-Feb-99
GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS *** 20 unordered pieces.	Homo sapiens	35,331	5-Nov-99
GB_HTG5:AC011678	171967	AC011678	Homo sapiens clone 14_B_7, *** SEQUENCING IN PROGRESS *** 20 unordered pieces.	Homo sapiens	33,807	5-Nov-99
GB_BA2:AF064070	23183	AF064070	Burkholderia pseudomallei putative dihydroorotase (pyrC) gene, partial cds; putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (plsC), putative diadenosine tetraphosphatase (apaH), complete cds; type II O-antigen biosynthesis gene cluster, complete sequence; putative undecaprenyl phosphate N-acetylglucosaminyltransferase, and putative UDP-glucose 4-epimerase genes, complete cds; and putative galactosyl transferase gene, partial cds.	Burkholderia pseudomallei	36,929	20-Jan-99
GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,852	14-Sep-98
GB_IN1:CELT1984	37121	U80438	Caenorhabditis elegans cosmid T19B4.	Caenorhabditis elegans	43,836	04-DEC-1996
GB_EST36:AV193572	360	AV193572	AV193572 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk618h8 5', mRNA sequence.	Caenorhabditis elegans	48,588	22-Jul-99
GB_BA2:AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dcIAE) gene, partial cds; adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds; and unknown gene.	Corynebacterium glutamicum	99,914	14-Sep-98
GB_BA1.MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome, segment 114/162.	Mycobacterium tuberculosis	38,339	17-Jun-98
GB_BA1:U00011	40429	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	38,996	01-MAR-1994
GB_BA1.MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome, segment 111/162.	Mycobacterium tuberculosis	37,640	17-Jun-98
GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,906	3-Jun-99
GB_PR4:AC006581	172931	AC006581	Homo sapiens 12p21 BAC RPC111-259O18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,280	3-Jun-99
GB_BA1.MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome, segment 111/162.	Mycobacterium tuberculosis	39,765	17-Jun-98
GB_OV:CHKCEK2	3694	M35195	Chicken tyrosine kinase (cek2) mRNA, complete cds.	Gallus gallus	38,937	28-Apr-93
GB_BA1:MSASDASK	5037	Z17372	M. smegmatis asd, ask-alpha, and ask-beta genes.	Mycobacterium smegmatis	38,495	9-Aug-94
GB_EST24:AI223401	169	AI223401	qg48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 3' similar to WP:C2507.8 CE08394, mRNA sequence.	Homo sapiens	40,828	27-OCT-1998

	Accession	Gene ID	Gene Name	Species	Date
α02814	GB_EST24.A1223401	169	ig48g01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838448 similar to WP.C25D7.8 CE08394., mRNA sequence.	Homo sapiens	27-OCT-1998
	GB_BA1.MTCY7D11	22070	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	17-Jun-98
	GB_BA1.MTCY7D11	22070	Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.	Mycobacterium tuberculosis	17-Jun-98
	GB_PR1.HSAJ2962	778	Homo sapiens mRNA for hB-FABP.	Homo sapiens	8-Jan-98
	GB_BA1.CG AJ4934	1160	Corynebacterium glutamicum dapD gene, complete CDS.	Corynebacterium glutamicum	17-Jun-98
	GB_BA1.MTCI364	29540	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	17-Jun-98
α03205	GB_BA1.MLU15180	38675	Mycobacterium leprae cosmid B1756.	Mycobacterium leprae	09-MAR-1995
	GB_BA1.BLSIGBN	2906	B.lactofermentum orf1 gene and sigB gene.	Corynebacterium glutamicum	25-Apr-96
	GB_EST21.AA980237	377	aa32a12.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1348414 5' similar to TR.Q61025 Q61025 HYPOTHETICAL 15.2 KD PROTEIN., mRNA sequence.	Mus musculus	27-MAY-1998
	GB_EST23.AI158316	371	ad27c05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1447112 5', mRNA sequence.	Mus musculus	30-Sep-98
α03223	GB_IN1.LMFL2743	38368	Leishmania major Friedlin chromosome 4 cosmid L2743.	Leishmania major	15-DEC-1999
	GB_PR3.HSDJ61B2	119666	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 230/240kD), an exon of a gene similar to murine MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	17-DEC-1999
	GB_PR3.HSDJ61B2	119666	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 230/240kD), an exon of a gene similar to m ne MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	17-DEC-1999
	GB_PR3.HSDJ61B2	119666	Human DNA sequence from clone RP1-61B2 on chromosome 6p11.2-12.3 Contains isoforms 1 and 3 of BPAG1 (bullous pemphigoid antigen 1 230/240kD), an exon of a gene similar to m ne MACF cytoskeletal protein, STSs and GSSs, complete sequence.	Homo sapiens	17-DEC-1999

### Exemplification

#### **Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032**

5           A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,  
10   2.46 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 10 ml/l  $\text{KH}_2\text{PO}_4$  solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l  $(\text{NH}_4)_2\text{SO}_4$ , 1 g/l NaCl, 2 g/l  $\text{MgSO}_4 \times 7\text{H}_2\text{O}$ , 0.2 g/l  $\text{CaCl}_2$ , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l  $\text{FeSO}_4 \times \text{H}_2\text{O}$ , 10 mg/l  $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$ , 3 mg/l  $\text{MnCl}_2 \times 4\text{H}_2\text{O}$ , 30 mg/l  $\text{H}_3\text{BO}_3$ , 20 mg/l  $\text{CoCl}_2 \times 6\text{H}_2\text{O}$ , 1 mg/l  $\text{NiCl}_2 \times 6\text{H}_2\text{O}$ , 3 mg/l  $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$ , 500 mg/l complexing agent  
15 (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting  
20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by  
25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20  
30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

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min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

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**Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.**

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

20

**Example 3: DNA Sequencing and Computational Functional Analysis**

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

25

**Example 4: *In vivo* Mutagenesis**

*In vivo* mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

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the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

**Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum***

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g., Martin, J.F. et al. (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. et al. (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see e.g., Yoshihama, M. et al. (1985) *J. Bacteriol.* 162:591-597, Martin J.F. et al. (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. et al. (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. et al. (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. et al. (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described e.g. in Schnafer, A et al.

(1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient  
5 *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be  
10 overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known  
15 methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as  
20 homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention, such terminators are well-known in the art and are described, for example, in  
Winnacker, E.L. (1987) *From Genes to Clones - Introduction to Gene Technology*. VCH:  
25 Weinheim.

#### **Example 6: Assessment of the Expression of the Mutant Protein**

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity  
30 to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

- (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.
- 10 To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which
- 15 specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

#### 20 **Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions**

- Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der
- 25 Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as
- 30 mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or  
5 ammonia salts, such as  $\text{NH}_4\text{Cl}$  or  $(\text{NH}_4)_2\text{SO}_4$ ,  $\text{NH}_4\text{OH}$ , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt,  
10 molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic  
15 acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A  
20 Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and  
121°C) or by sterile filtration. The components can either be sterilized together or, if  
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to  
30 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH<sub>4</sub>OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD<sub>600</sub> of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

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### **Example 8 – *In vitro* Analysis of the Function of Mutant Proteins**

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

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found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3<sup>rd</sup> ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2<sup>nd</sup> ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3<sup>rd</sup> ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

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#### **Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product**

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

- Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

#### **Example 10: Purification of the Desired Product from *C. glutamicum* Culture**

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

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cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotechnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. *Ulmann's Encyclopedia of Industrial Chemistry*, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

### Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

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were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a  
5 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the  
10 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP  
15 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For  
20 example, a value of "40,345" in this column represents "40.345%".

#### **Example 12: Construction and Operation of DNA Microarrays**

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are  
25 well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose,  
30 nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the

5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice

10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide

15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the

20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be

25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),

30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

### **Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)**

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and  
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*,  $^{35}\text{S}$ -methionine,  $^{35}\text{S}$ -cysteine,  $^{14}\text{C}$ -labelled amino acids,  $^{15}\text{N}$ -amino acids,  $^{15}\text{NO}_3$  or  $^{15}\text{NH}_4^+$  or  $^{13}\text{C}$ -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,  
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount  
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other  
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,  
30 such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

**Equivalents**

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a  
5 metabolic pathway protein, or a portion thereof, provided that the nucleic acid  
molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway  
protein is selected from the group consisting of proteins involved in the metabolism  
10 of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or  
trehalose.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the  
group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the  
15 Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does  
not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected  
from the group consisting of those sequences set forth as even-numbered SEQ ID  
20 NOs of the Sequence Listing, provided that the nucleic acid molecule does not  
consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant  
of a polypeptide selected from the group of amino acid sequences consisting of those  
25 sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,  
provided that the nucleic acid molecule does not consist of any of the F-designated  
genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least  
30 50% homologous to a nucleotide sequence selected from the group consisting of  
those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

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a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides  
5 of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 10 8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous  
15 polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
- 20 12. A host cell transfected with the expression vector of claim 11.
- ~~13. The host cell of claim 12, wherein said cell is a microorganism.~~
- 25 14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
- 30 16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine

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bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12  
5 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated metabolic pathway polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 10 19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the metabolism of an amino acid, a vitamin, a cofactor, a nutraceutical, a nucleotide, a nucleoside, or trehalose.
20. An isolated polypeptide comprising an amino acid sequence selected from the group  
15 consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
21. An isolated polypeptide comprising a naturally occurring allelic variant of a  
20 polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.
23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a  
30 nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

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24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,  
5 provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.  
10
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
27. The method of claim 25, wherein said method further comprises the step of  
15 transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.  
20
29. The method of claim 25, wherein said cell is selected from the group consisting of:  
*Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*,  
*Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*,  
*Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium*  
25 *fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,  
*Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*,  
*Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium*  
*ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*,  
*Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.  
30
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through 1156 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence Listing, wherein the nucleic acid molecule comprises one or more nucleic acid

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modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of  
5 the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing , wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

## SEQUENCE LISTING

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 Leu Thr Ile Pro Phe  
 1 5  
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 Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu  
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 gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac 211  
 Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp  
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 Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala  
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 gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat 307  
 Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp  
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 Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val  
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 Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu  
 105 110 115  
 cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct 499  
 Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro  
 120 125 130  
 gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547  
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150	155	160	165
ggc tta agt gcg tgc gct ctt gcc gat atg gaa ctg cgc gca cct acg			643
Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr			
	170	175	180
ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca			691
Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr			
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gaa tta gaa gat gac gca gta tgc atg cgc gtg tgg gaa cgc gga gtg			739
Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val			
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Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala			
	215	220	225
gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt			835
Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val			
	230	235	240
cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc			883
Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu			
	250	255	260
acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc			925
Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile			
	265	270	275
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&lt;210&gt; 2

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 2

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	20	25	30
Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu			
	35	40	45
Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser			
	50	55	60
Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met			
	65	70	75
Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly			
	85	90	95

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 His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val  
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 Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu  
 145 150 155 160  
 Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu  
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 180 185 190  
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 195 200 205  
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 225 230 235 240  
 Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp  
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 Val Gln Ile  
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 1 5  
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
 10 15 20  
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
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70 75 80 85	
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ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Asn Gly Gly	
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
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Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
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 295 300 305

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 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
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 1123  
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 330 335 340

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 1171  
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 345 350 355

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 1219  
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 360 365 370

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 1267  
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 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
 1363  
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 410 415 420

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 425 430 435

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 440 445 450

gcg ttg ttc taagttttct agataacaag gcc  
 1491  
 Ala Leu Phe  
 455

&lt;211&gt; 456

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 4

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
 1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser  
405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu  
420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu  
435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe  
450 455

<210> 5

<211> 1330

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 5

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ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115  
Leu Ala Leu Lys Gly  
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
1027

Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
1075

Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
1123

Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
1171

Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
1219

Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
1267

Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
390 395 400 405

ttc aag gaa cgc ggc  
1330

Phe Lys Glu Arg Gly  
410

<210> 6

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 6

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly  
405 410

<210> 7

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXC02390

<400> 7

gctgggtgtg ctgacccata cgctggaact ccaactgctg ttgataccgc caagatgttt 60

ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct 115  
Val Glu Trp Thr Ala  
1 5

ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163  
Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly  
10 15 20

cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac 211  
Pro Asp Thr Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His  
25 30 35

gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg 259  
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val  
40 45 50

acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg 307  
Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser  
55 60 65

att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att 355  
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile  
70 75 80 85

ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc 403  
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg  
90 95 100

cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa 451  
Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu  
105 110 115

gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac 499  
Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn  
120 125 130

ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg 547  
Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro  
135 140 145

ttc atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg 595  
Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val  
150 155 160 165

gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att 643  
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile  
                   170                                  175                                  180

gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg 691  
 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp  
                   185                                  190                                  195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg 739  
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu  
                   200                                  205                                  210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct 789  
 Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly  
                   215                                  220

tcc 792

<210> 8

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly  
           1                                  5                                  10                                  15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr  
                   20                                  25                                  30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly  
                   35                                  40                                  45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu  
           50                                  55                                  60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr  
           65                                  70                                  75                                  80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu  
                   85                                  90                                  95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile  
                   100                                  105                                  110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln  
                   115                                  120                                  125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala  
           130                                  135                                  140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala  
           145                                  150                                  155                                  160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser  
                   165                                  170                                  175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu  
                   180                                  185                                  190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val  
 195 200 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly  
 210 215 220

<210> 9

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXC01796

<400> 9

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ttggtgcggc atcgggtggcc tgctactagt cgggctcttc ttg ctc ctt ggc ggt 115  
 Leu Leu Leu Gly Gly  
 1 5

aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc 163  
 Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile  
 10 15 20

gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc 211  
 Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr  
 25 30 35

ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259  
 Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser  
 40 45 50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt 307  
 Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly  
 55 60 65

atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa 355  
 Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln  
 70 75 80 85

acc ggc tgc ggt ttc gct tct gcg tcc act ggc ccg ttt tac tgt ccg 403  
 Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro  
 90 95 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451  
 Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg  
 105 110 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg 499  
 Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala  
 120 125 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547  
 His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu  
 135 140 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag 595

Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu  
 150 155 160 165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa 643  
 Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu  
 170 175 180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691  
 Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser  
 185 190 195

gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga 739  
 Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg  
 200 205 210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag 787  
 Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln  
 215 220 225

cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc 835  
 Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser  
 230 235 240 245

gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884  
 Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala  
 250 255

cttttcgacg tct 897

&lt;210&gt; 10

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 10

Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly  
 1 5 10 15

Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe  
 20 25 30

Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg  
 35 40 45

Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu  
 50 55 60

Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe  
 65 70 75 80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly  
 85 90 95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe  
 100 105 110

Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln  
 115 120 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu

130	135	140
Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn		
145	150	155 160
Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala		
	165	170 175
Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu		
	180	185 190
Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp		
	195	200 205
Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr		
	210	215 220
His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn		
	225	230 235 240
Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn		
	245	250 255

Asp Ala

<210> 11  
 <211> 771  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(748)  
 <223> RXC01207

<400> 11  
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atTTTTgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115  
 Val Ser Arg Ile Tyr  
 1 5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163  
 Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val  
 10 15 20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211  
 Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu  
 25 30 35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259  
 Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu  
 40 45 50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307  
 Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val  
 55 60 65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355

Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln  
 70 75 80 85  
 gag aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403  
 Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile  
 90 95 100  
 gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451  
 Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly  
 105 110 115  
 acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499  
 Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu  
 120 125 130  
 cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547  
 Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His  
 135 140 145  
 act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595  
 Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn  
 150 155 160 165  
 gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643  
 Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser  
 170 175 180  
 acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691  
 Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly  
 185 190 195  
 gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739  
 Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu  
 200 205 210  
 agc ctg cgc taaatgggag tcggtttcgc ggg 771  
 Ser Leu Arg  
 215

&lt;210&gt; 12

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly  
 1 5 10 15  
 Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu  
 20 25 30  
 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu  
 35 40 45  
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro  
 50 55 60  
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His  
 65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly  
85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu  
100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val  
115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala  
130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln  
145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala  
165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys  
180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu  
195 200 205

Gly Val Ser Ala Glu Ser Leu Arg  
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<210> 13

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXC00657

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Met Ser Thr Glu Asp  
1 5

att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163  
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val  
10 15 20

cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211  
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu  
25 30 35

gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259  
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val  
40 45 50

cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag 307  
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys  
55 60 65

att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag 355  
 Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys  
 70 75 80 85

atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa 403  
 Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu  
 90 95 100

atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc 451  
 Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly  
 105 110 115

gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc 499  
 Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser  
 120 125 130

cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac 547  
 His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn  
 135 140 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595  
 Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu  
 150 155 160 165

gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt 643  
 Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg  
 170 175 180

ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag 691  
 Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln  
 185 190 195

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739  
 Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val  
 200 205 210

gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg 787  
 Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val  
 215 220 225

gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835  
 Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg  
 230 235 240 245

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883  
 Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val  
 250 255 260

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931  
 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser  
 265 270 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979  
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val  
 280 285 290

cgc cca cct gag aag att aag aag tagttttcttt taagtttcca tgc  
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 Arg Pro Pro Glu Lys Ile Lys Lys  
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<210> 14  
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 <213> Corynebacterium glutamicum

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           20                    25                    30  
 Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr  
           35                    40                    45  
 Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala  
           50                    55                    60  
 Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val  
           65                    70                    75                    80  
 Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile  
                     85                    90                    95  
 Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly  
                     100                    105                    110  
 Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser  
           115                    120                    125  
 Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu  
           130                    135                    140  
 Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly  
           145                    150                    155                    160  
 Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala  
                     165                    170                    175  
 Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met  
           180                    185                    190  
 Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln  
           195                    200                    205  
 Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg  
           210                    215                    220  
 Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile  
           225                    230                    235                    240  
 Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn  
                     245                    250                    255  
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly  
           260                    265                    270  
 Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys  
           275                    280                    285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys  
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 <213> Corynebacterium glutamicum

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 Val Ala Thr Ser Lys  
 1 5  
 att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163  
 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val  
 10 15 20  
 cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc 211  
 Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg  
 25 30 35  
 atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att 259  
 Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile  
 40 45 50  
 gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc 307  
 Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe  
 55 60 65  
 aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca 355  
 Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro  
 70 75 80 85  
 aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca 403  
 Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro  
 90 95 100  
 gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac 451  
 Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Val His  
 105 110 115  
 ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa 499  
 Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu  
 120 125 130  
 gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag 547  
 Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys  
 135 140 145  
 ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc 595  
 Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile  
 150 155 160 165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg 643  
 Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val  
 170 175 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc 691  
 Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu  
 185 190 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc 739  
 Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile  
 200 205 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc 787  
 Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser  
 215 220 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac 835  
 Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr  
 230 235 240 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt 883  
 Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe  
 250 255 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931  
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys  
 265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979  
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg  
 280 285 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc  
 1027  
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu  
 295 300 305

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 1059  
 Val Thr Ser  
 310

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 <213> Corynebacterium glutamicum

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 Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr  
 35 40 45  
 Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg  
 50 55 60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly  
 65 70 75 80  
 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val  
 85 90 95  
 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val  
 100 105 110  
 Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu  
 115 120 125  
 Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu  
 130 135 140  
 Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr  
 145 150 155 160  
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu  
 165 170 175  
 Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu  
 180 185 190  
 Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln  
 195 200 205  
 Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly  
 210 215 220  
 Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu  
 225 230 235 240  
 Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr  
 245 250 255  
 Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu  
 260 265 270  
 Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His  
 275 280 285

Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln  
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Gly Ile Asp Pro Leu Val Thr Ser  
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<210> 17  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1555)  
 <223> RXN00351

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Met Asp Asp Ser Asn  
1 5

agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac 163  
Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His  
10 15 20

cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg 211  
Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr  
25 30 35

ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg 259  
Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp  
40 45 50

cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt 307  
Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly  
55 60 65

gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc 355  
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe  
70 75 80 85

tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg 403  
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu  
90 95 100

att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag 451  
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu  
105 110 115

gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt 499  
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly  
120 125 130

gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att 547  
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile  
135 140 145

ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att 595  
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile  
150 155 160 165

ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag 643  
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu  
170 175 180

att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt 691  
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val  
185 190 195

caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act 739  
Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr  
200 205 210

gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa 787  
Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu  
215 220 225

gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg 835  
 Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg  
 230 235 240 245

cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt 883  
 Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe  
 250 255 260

ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac 931  
 Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp  
 265 270 275

gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag 979  
 Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys  
 280 285 290

ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc  
 1027  
 Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly  
 295 300 305

gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg  
 1075  
 Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser  
 310 315 320 325

cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa  
 1123  
 Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu  
 330 335 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg  
 1171  
 Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val  
 345 350 355

gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg  
 1219  
 Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu  
 360 365 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg  
 1267  
 Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met  
 375 380 385

aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt  
 1315  
 Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly  
 390 395 400 405

gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt  
 1363  
 Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly  
 410 415 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg  
 1411  
 Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met  
 425 430 435

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg  
1459

Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr  
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg  
1507

Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val  
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac tca  
1555

Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn Ser  
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1578

<210> 18

<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

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20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly  
35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe  
50 55 60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser  
65 70 75 80

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro  
85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp  
100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln  
115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu  
130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly  
145 150 155 160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu  
165 170 175

Pro Trp Arg Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val  
180 185 190

Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln  
 195 200 205  
 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu  
 210 215 220  
 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu  
 225 230 235 240  
 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile  
 245 250 255  
 Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu  
 260 265 270  
 Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg  
 275 280 285  
 Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu  
 290 295 300  
 Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln  
 305 310 315 320  
 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg  
 325 330 335  
 Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg  
 340 345 350  
 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn  
 355 360 365  
 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro  
 370 375 380  
 Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His  
 385 390 395 400  
 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala  
 405 410 415  
 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser  
 420 425 430  
 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro  
 435 440 445  
 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr  
 450 455 460  
 His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln  
 465 470 475 480  
 Ser Gly Glu Asn Ser  
 485

<210> 19  
 <211> 1546  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1546)

&lt;223&gt; FRXA00351

&lt;400&gt; 19

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cgcaaagaag accacaaaga agtccttaagc cggatcttat	atg gat gat tcc aat	115
	Met Asp Asp Ser Asn	
	1 5	

agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc cac	163
Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val His	
10 15 20	

cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc acg	211
Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val Thr	
25 30 35	

ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga tgg	259
Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly Trp	
40 45 50	

cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg ggt	307
Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr Gly	
55 60 65	

ggt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc ttc	355
Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly Phe	
70 75 80 85	

tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat ctg	403
Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp Leu	
90 95 100	

att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cgg gag	451
Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg Glu	
105 110 115	

gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac ggt	499
Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His Gly	
120 125 130	

gcc act gtg tgg gtg cag gac tat cag ctg ttg ctg gtt cct ggc att	547
Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Leu Val Pro Gly Ile	
135 140 145	

ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac att	595
Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His Ile	
150 155 160 165	

ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa gag	643
Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu Glu	
170 175 180	

att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg gtt	691
Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu Val	
185 190 195	

caa aac gca gaa aac ttc ctt gcg tta acc cag cag gtt gcc ggc act 739  
 Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly Thr  
 200 205 210

gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt gaa 787  
 Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly Glu  
 215 220 225

gca ttg gtg cgt gag att ggc gct cat gtt gaa acc gct gac gga agg 835  
 Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly Arg  
 230 235 240 245

cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg ttt 883  
 Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met Phe  
 250 255 260

ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc gac 931  
 Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu Asp  
 265 270 275

gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc aag 979  
 Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr Lys  
 280 285 290

ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc ggc  
 1027  
 Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser Gly  
 295 300 305

gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct tcg  
 1075  
 Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro Ser  
 310 315 320 325

cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag gaa  
 1123  
 Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu Glu  
 330 335 340

gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc gtg  
 1171  
 Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro Val  
 345 350 355

gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg ctg  
 1219  
 Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val Leu  
 360 365 370

tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt atg  
 1267  
 Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly Met  
 375 380 385

aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act ggt  
 1315  
 Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr Gly  
 390 395 400 405

gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc ggt  
1363

Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr Gly  
410 415 420

gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa atg  
1411

Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln Met  
425 430 435

gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca acg  
1459

Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala Thr  
440 445 450

cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac gtg  
1507

Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn Val  
455 460 465

tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga  
1546

Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly  
470 475 480

<210> 20

<211> 482

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val  
1 5 10 15

Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro  
20 25 30

Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly  
35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe  
50 55 60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser  
65 70 75 80

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro  
85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp  
100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln  
115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu  
130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly  
145 150 155 160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu  
 165 170 175  
 Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val  
 180 185 190  
 Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln  
 195 200 205  
 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu  
 210 215 220  
 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu  
 225 230 235 240  
 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile  
 245 250 255  
 Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu  
 260 265 270  
 Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg  
 275 280 285  
 Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu  
 290 295 300  
 Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln  
 305 310 315 320  
 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg  
 325 330 335  
 Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg  
 340 345 350  
 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn  
 355 360 365  
 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro  
 370 375 380

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Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His  
 385 390 395 400  
 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala  
 405 410 415  
 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser  
 420 425 430  
 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro  
 435 440 445  
 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr  
 450 455 460  
 His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln  
 465 470 475 480

Ser Gly

<210> 21  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(756)  
 <223> RXA00873

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 Thr Ala Gln Trp Gly Ile Phe Leu Arg Asn His Asp Glu Leu Thr Leu  
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gaa atg gtc tcc gat gag gaa cgc agc tac atg tac tcc caa ttc gcc 96  
 Glu Met Val Ser Asp Glu Glu Arg Ser Tyr Met Tyr Ser Gln Phe Ala  
                   20                  25                  30

tcc gaa cct cgc atg cgc gcc aac gta gga atc cgc agg cgc ctt tcc 144  
 Ser Glu Pro Arg Met Arg Ala Asn Val Gly Ile Arg Arg Arg Leu Ser  
           35                  40                  45

cca ctg ctt gaa ggc gac cgc aac cag ctg gaa ctc ctt cac ggt ttg 192  
 Pro Leu Leu Glu Gly Asp Arg Asn Gln Leu Glu Leu Leu His Gly Leu  
           50                  55                  60

ttg ctg tct cta cct ggc tca ccc gtg ttg tat tac ggt gat gaa att 240  
 Leu Leu Ser Leu Pro Gly Ser Pro Val Leu Tyr Tyr Gly Asp Glu Ile  
           65                  70                  75                  80

ggc atg ggc gac aat atc tgg ctc cac gac cgc gac gga gtg cgc acc 288  
 Gly Met Gly Asp Asn Ile Trp Leu His Asp Arg Asp Gly Val Arg Thr  
                   85                  90                  95

ccc atg cag tgg tcc aac gac cgc aac ggt ggt ttc tcc aaa gct gat 336  
 Pro Met Gln Trp Ser Asn Asp Arg Asn Gly Gly Phe Ser Lys Ala Asp  
           100                  105                  110

cct gaa cgc ctg tac ctt cca gcg atc caa aat gat caa tac ggc tac 384  
 Pro Glu Arg Leu Tyr Leu Pro Ala Ile Gln Asn Asp Gln Tyr Gly Tyr  
           115                  120                  125

gcc caa gta aac gtg gaa agc caa ctc aac cgc gaa aac tcc ctg ctg 432  
 Ala Gln Val Asn Val Glu Ser Gln Leu Asn Arg Glu Asn Ser Leu Leu  
           130                  135                  140

cgc tgg ctc cga aac caa atc ctt atc cgc aag cag tac cgc gca ttt 480  
 Arg Trp Leu Arg Asn Gln Ile Leu Ile Arg Lys Gln Tyr Arg Ala Phe  
           145                  150                  155                  160

ggt gcc gga acc tac cgt gaa gtg tcc tcc acc aat gag tca gtg ttg 528  
 Gly Ala Gly Thr Tyr Arg Glu Val Ser Ser Thr Asn Glu Ser Val Leu  
                   165                  170                  175

aca ttt tta cga gaa cac aag ggc caa acc att ttg tgt gtc aac aac 576  
 Thr Phe Leu Arg Glu His Lys Gly Gln Thr Ile Leu Cys Val Asn Asn

180	185	190	
atg agc aaa tat cct cag gca gtc tcg ctt gat ttg cgt gaa ttt gca			624
Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala			
195	200	205	
gga cac acc cct cga gag atg tcg ggc ggg cag ctg ttc cct acc att			672
Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile			
210	215	220	
gct gaa cgg gag tgg att gtc act tta gcc cct cac gga ttc ttc tgg			720
Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp			
225	230	235	240
ttt gat ctc acc gcc gat gaa aag gac gat atg gaa tgagcattgg			766
Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu			
245	250		
ccaacacatc atc			779

&lt;210&gt; 22

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 22

Thr	Ala	Gln	Trp	Gly	Ile	Phe	Leu	Arg	Asn	His	Asp	Glu	Leu	Thr	Leu
1				5					10				15		

Glu	Met	Val	Ser	Asp	Glu	Glu	Arg	Ser	Tyr	Met	Tyr	Ser	Gln	Phe	Ala
		20					25						30		

Ser	Glu	Pro	Arg	Met	Arg	Ala	Asn	Val	Gly	Ile	Arg	Arg	Arg	Leu	Ser
		35					40					45			

Pro	Leu	Leu	Glu	Gly	Asp	Arg	Asn	Gln	Leu	Glu	Leu	Leu	His	Gly	Leu
	50				55						60				

Leu	Leu	Ser	Leu	Pro	Gly	Ser	Pro	Val	Leu	Tyr	Tyr	Gly	Asp	Glu	Ile
	65				70					75					80

Gly	Met	Gly	Asp	Asn	Ile	Trp	Leu	His	Asp	Arg	Asp	Gly	Val	Arg	Thr
				85					90				95		

Pro	Met	Gln	Trp	Ser	Asn	Asp	Arg	Asn	Gly	Gly	Phe	Ser	Lys	Ala	Asp
		100						105					110		

Pro	Glu	Arg	Leu	Tyr	Leu	Pro	Ala	Ile	Gln	Asn	Asp	Gln	Tyr	Gly	Tyr
		115					120					125			

Ala	Gln	Val	Asn	Val	Glu	Ser	Gln	Leu	Asn	Arg	Glu	Asn	Ser	Leu	Leu
	130						135				140				

Arg	Trp	Leu	Arg	Asn	Gln	Ile	Leu	Ile	Arg	Lys	Gln	Tyr	Arg	Ala	Phe
	145				150					155					160

Gly	Ala	Gly	Thr	Tyr	Arg	Glu	Val	Ser	Ser	Thr	Asn	Glu	Ser	Val	Leu
			165						170					175	

Thr	Phe	Leu	Arg	Glu	His	Lys	Gly	Gln	Thr	Ile	Leu	Cys	Val	Asn	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180 185 190

Met Ser Lys Tyr Pro Gln Ala Val Ser Leu Asp Leu Arg Glu Phe Ala  
195 200 205

Gly His Thr Pro Arg Glu Met Ser Gly Gly Gln Leu Phe Pro Thr Ile  
210 215 220

Ala Glu Arg Glu Trp Ile Val Thr Leu Ala Pro His Gly Phe Phe Trp  
225 230 235 240

Phe Asp Leu Thr Ala Asp Glu Lys Asp Asp Met Glu  
245 250

<210> 23  
<211> 1102  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1102)  
<223> RXA00891

<400> 23  
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gaaagaccgc ctacgcattg tgcgcctggc tttttagaat gtg ctg caa acc tcc 115  
Val Leu Gln Thr Ser  
1 5

tgg cat ttc tct atc ctg gca ggc atg act gat acc tct ccg ttg aat 163  
Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp Thr Ser Pro Leu Asn  
10 15 20

tct cag ccg agt gca gat cac cac cct gat cac gcg gct cgc cca gtt 211  
Ser Gln Pro Ser Ala Asp His His Pro Asp His Ala Ala Arg Pro Val  
25 30 35

ctt gat gcc cac ggc ttg atc gtt gag cac gaa tcg gaa gag ttt cca 259  
Leu Asp Ala His Gly Leu Ile Val Glu His Glu Ser Glu Glu Phe Pro  
40 45 50

gtc ccc gca ccc gct ccc ggt gaa cag ccc tgg gag aag aaa aac cgc 307  
Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp Glu Lys Lys Asn Arg  
55 60 65

gag tgg tac aaa gac gcc gtt ttc tac gaa gtg ctg gtt cgt gcc ttc 355  
Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val Leu Val Arg Ala Phe  
70 75 80 85

tac gat cca gaa ggc aac gga gtc gga tcg ttg aaa ggc ctg acc gaa 403  
Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu Lys Gly Leu Thr Glu  
90 95 100

aaa ctg gat tac atc cag tgg ctc ggc gtg gat tgc att tgg atc cca 451  
Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp Cys Ile Trp Ile Pro  
105 110 115

ccg ttt tat gat tcc cca ctg cgc gac ggc ggt tac gat atc cgc aac 499

Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly Tyr Asp Ile Arg Asn  
 120 125 130

ttc cgt gaa atc ctg ccc gaa ttc ggc acc gtc gat gac ttc gtg gaa 547  
 Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val Asp Asp Phe Val Glu  
 135 140 145

ctc gtt gac cac gcc cac cgc cgt ggc ctg cgt gtt atc acc gac ttg 595  
 Leu Val Asp His Ala His Arg Arg Gly Leu Arg Val Ile Thr Asp Leu  
 150 155 160 165

gtc atg aat cac acc tcc gac cag cac gca tgg ttc caa gaa tcc cgg 643  
 Val Met Asn His Thr Ser Asp Gln His Ala Trp Phe Gln Glu Ser Arg  
 170 175 180

cgc gac cca acc ggc ccc tac gga gat ttc tat gtg tgg agc gat gat 691  
 Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr Val Trp Ser Asp Asp  
 185 190 195

ccc acc ctg tac aac gaa gcc cgc atc atc ttt gta gat aca gaa gaa 739  
 Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe Val Asp Thr Glu Glu  
 200 205 210

tcc aac tgg acc tat gat ccg gtg cgt ggc cag tac ttc tgg cac cgc 787  
 Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln Tyr Phe Trp His Arg  
 215 220 225

ttc ttc tcc cac caa cca gac ctc aac tac gac aac ccc gca gtc caa 835  
 Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp Asn Pro Ala Val Gln  
 230 235 240 245

gag gcc atg cta gat gtc ttg cgt ttc tgg ctg gac ctg gga ctt gat 883  
 Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu Asp Leu Gly Leu Asp  
 250 255 260

ggc ttc cga cta gat gcc gtt cct tat ctt ttt gaa cgc gaa ggc acc 931  
 Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe Glu Arg Glu Gly Thr  
 265 270 275

aac ggc gaa aac ctc aaa gaa acc cac gat ttc ctc aaa ctg tgt cgc 979  
 Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe Leu Lys Leu Cys Arg  
 280 285 290

tct gtc att gag aag gaa tac ccc ggc cga atc ctg ctc gca gaa gcc  
 1027  
 Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile Leu Leu Ala Glu Ala  
 295 300 305

aac caa tgg ccc caa gat gtg gtc gaa tac ttc ggt gaa aaa gac aaa  
 1075  
 Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe Gly Glu Lys Asp Lys  
 310 315 320 325

ggc gat gaa tgc cac atg gcc ttc cac  
 1102  
 Gly Asp Glu Cys His Met Ala Phe His  
 330

<210> 24

<211> 334

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 24

Val Leu Gln Thr Ser Trp His Phe Ser Ile Leu Ala Gly Met Thr Asp  
 1 5 10 15

Thr Ser Pro Leu Asn Ser Gln Pro Ser Ala Asp His His Pro Asp His  
 20 25 30

Ala Ala Arg Pro Val Leu Asp Ala His Gly Leu Ile Val Glu His Glu  
 35 40 45

Ser Glu Glu Phe Pro Val Pro Ala Pro Ala Pro Gly Glu Gln Pro Trp  
 50 55 60

Glu Lys Lys Asn Arg Glu Trp Tyr Lys Asp Ala Val Phe Tyr Glu Val  
 65 70 75 80

Leu Val Arg Ala Phe Tyr Asp Pro Glu Gly Asn Gly Val Gly Ser Leu  
 85 90 95

Lys Gly Leu Thr Glu Lys Leu Asp Tyr Ile Gln Trp Leu Gly Val Asp  
 100 105 110

Cys Ile Trp Ile Pro Pro Phe Tyr Asp Ser Pro Leu Arg Asp Gly Gly  
 115 120 125

Tyr Asp Ile Arg Asn Phe Arg Glu Ile Leu Pro Glu Phe Gly Thr Val  
 130 135 140

Asp Asp Phe Val Glu Leu Val Asp His Ala His Arg Arg Gly Leu Arg  
 145 150 155 160

Val Ile Thr Asp Leu Val Met Asn His Thr Ser Asp Gln His Ala Trp  
 165 170 175

Phe Gln Glu Ser Arg Arg Asp Pro Thr Gly Pro Tyr Gly Asp Phe Tyr  
 180 185 190

Val Trp Ser Asp Asp Pro Thr Leu Tyr Asn Glu Ala Arg Ile Ile Phe  
 195 200 205

Val Asp Thr Glu Glu Ser Asn Trp Thr Tyr Asp Pro Val Arg Gly Gln  
 210 215 220

Tyr Phe Trp His Arg Phe Phe Ser His Gln Pro Asp Leu Asn Tyr Asp  
 225 230 235 240

Asn Pro Ala Val Gln Glu Ala Met Leu Asp Val Leu Arg Phe Trp Leu  
 245 250 255

Asp Leu Gly Leu Asp Gly Phe Arg Leu Asp Ala Val Pro Tyr Leu Phe  
 260 265 270

Glu Arg Glu Gly Thr Asn Gly Glu Asn Leu Lys Glu Thr His Asp Phe  
 275 280 285

Leu Lys Leu Cys Arg Ser Val Ile Glu Lys Glu Tyr Pro Gly Arg Ile  
 290 295 300

Leu Leu Ala Glu Ala Asn Gln Trp Pro Gln Asp Val Val Glu Tyr Phe  
305 310 315 320

Gly Glu Lys Asp Lys Gly Asp Glu Cys His Met Ala Phe His  
325 330

<210> 25

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXA00534

<400> 25

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gcgggtaact gtcagcacgt agatcgaaag gtgcacaaag gtg gcc ctg gtc gta 115  
Val Ala Leu Val Val  
1 5

cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac 163  
Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn  
10 15 20

gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg 211  
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val  
25 30 35

gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt 259  
Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu  
40 45 50

gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc 307  
Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu  
55 60 65

ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355  
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile  
70 75 80 85

gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt 403  
Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly  
90 95 100

gtg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act 451  
Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr  
105 110 115

cca ggt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt 499  
Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val  
120 125 130

gct ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg 547  
Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu  
135 140 145

ggc cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg 595

Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Leu Ala Ala Ala Leu  
 150 155 160 165

aac gct gat gtg tgt gag att tac tcg gac gtt gac ggt gtg tat acc 643  
 Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val Asp Gly Val Tyr Thr  
 170 175 180

gct gac ccg cgc atc gtt cct aat gca cag aag ctg gaa aag ctc agc 691  
 Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys Leu Glu Lys Leu Ser  
 185 190 195

ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc tcc aag att ttg gtg 739  
 Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly Ser Lys Ile Leu Val  
 200 205 210

ctg cgc agt gtt gaa tac gct cgt gca ttc aat gtg cca ctt cgc gta 787  
 Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn Val Pro Leu Arg Val  
 215 220 225

cgc tcg tct tat agt aat gat ccc ggc act ttg att gcc ggc tct atg 835  
 Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu Ile Ala Gly Ser Met  
 230 235 240 245

gag gat att cct gtg gaa gaa gca gtc ctt acc ggt gtc gca acc gac 883  
 Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp  
 250 255 260

aag tcc gaa gcc aaa gta acc gtt ctg ggt att tcc gat aag cca ggc 931  
 Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly  
 265 270 275

gag gct gcg aag gtt ttc cgt gcg ttg gct gat gca gaa atc aac att 979  
 Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile  
 280 285 290

gac atg gtt ctg cag aac gtc tct tct gta gaa gac ggc acc acc gac  
 1027  
 Asp Met Val Leu Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp  
 295 300 305

atc acc ttc acc tgc cct cgt tcc gac ggc cgc cgc gcg atg gag atc  
 1075  
 Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg Arg Ala Met Glu Ile  
 310 315 320 325

ttg aag aag ctt cag gtt cag ggc aac tgg acc aat gtg ctt tac gac  
 1123  
 Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp  
 330 335 340

gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct ggc atg aag tct cac  
 1171  
 Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His  
 345 350 355

cca ggt gtt acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg  
 1219  
 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val  
 360 365 370

aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc  
1267

Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile  
375 380 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc  
1315

Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe  
390 395 400 405

cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc  
1363

Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg  
410 415 420

taaagtttta aaggagtagt ttt  
1386

<210> 26

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
 195 200 205  
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220  
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240  
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
 245 250 255  
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
 260 265 270  
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
 275 280 285  
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
 290 295 300  
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
 305 310 315 320  
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 325 330 335  
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 340 345 350  
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 355 360 365  
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
 370 375 380  
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Arg Ala  
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 Met Thr Thr Ile Ala

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gtt	gtt	ggt	gca	acc	ggc	cag	gtc	ggc	cag	gtt	atg	cgc	acc	ctt	ttg	163	
Val	Val	Gly	Ala	Thr	Gly	Gln	Val	Gly	Gln	Val	Met	Arg	Thr	Leu	Leu		
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gaa	gag	cgc	aat	ttc	cca	gct	gac	act	gtt	cgt	ttc	ttt	gct	tcc	cca	211	
Glu	Glu	Arg	Asn	Phe	Pro	Ala	Asp	Thr	Val	Arg	Phe	Phe	Ala	Ser	Pro		
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cgt	tcc	gca	ggc	cgt	aag	att	gaa	ttc	cgt	ggc	acg	gaa	atc	gag	gta	259	
Arg	Ser	Ala	Gly	Arg	Lys	Ile	Glu	Phe	Arg	Gly	Thr	Glu	Ile	Glu	Val		
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gaa	gac	att	act	cag	gca	acc	gag	gag	tcc	ctc	aag	gac	atc	gac	gtt	307	
Glu	Asp	Ile	Thr	Gln	Ala	Thr	Glu	Glu	Ser	Leu	Lys	Asp	Ile	Asp	Val		
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gcg	ttg	ttc	tcc	gct	gga	ggc	acc	gct	tcc	aag	cag	tac	gct	cca	ctg	355	
Ala	Leu	Phe	Ser	Ala	Gly	Gly	Thr	Ala	Ser	Lys	Gln	Tyr	Ala	Pro	Leu		
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ttc	gct	gct	gca	ggc	gcg	act	gtt	gtg	gat	aac	tct	tct	gct	tgg	cgc	403	
Phe	Ala	Ala	Ala	Gly	Ala	Thr	Val	Val	Asp	Asn	Ser	Ser	Ala	Trp	Arg		
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aag	gac	gac	gag	gtt	cca	cta	atc	gtc	tct	gag	gtg	aac	cct	tcc	gac	451	
Lys	Asp	Asp	Glu	Val	Pro	Leu	Ile	Val	Ser	Glu	Val	Asn	Pro	Ser	Asp		
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Lys	Asp	Ser	Leu	Val	Lys	Gly	Ile	Ile	Ala	Asn	Pro	Asn	Cys	Thr	Thr		
				120					125					130			
atg	gct	gcg	atg	cca	gtg	ctg	aag	cca	ctt	cac	gat	gcc	gct	ggt	ctt	547	
Met	Ala	Ala	Met	Pro	Val	Leu	Lys	Pro	Leu	His	Asp	Ala	Ala	Gly	Leu		
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gta	aag	ctt	cac	gtt	tcc	tct	tac	cag	gct	gtt	tcc	ggt	tct	ggt	ctt	595	
Val	Lys	Leu	His	Val	Ser	Ser	Tyr	Gln	Ala	Val	Ser	Gly	Ser	Gly	Leu		
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gca	ggc	gtg	gaa	acc	ttg	gca	aag	cag	gtt	gct	gca	gtt	gga	gac	cac	643	
Ala	Gly	Val	Glu	Thr	Leu	Ala	Lys	Gln	Val	Ala	Ala	Val	Gly	Asp	His		
				170					175					180			
aac	gtt	gag	ttc	gtc	cat	gat	gga	cag	gct	gct	gac	gca	ggc	gat	gtc	691	
Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	Asp	Ala	Gly	Asp	Val		
				185					190					195			
gga	cct	tat	gtt	tca	cca	atc	gct	tac	aac	gtg	ctg	cca	ttc	gcc	gga	739	
Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	Leu	Pro	Phe	Ala	Gly		
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aac	ctc	gtc	gat	gac	ggc	acc	ttc	gaa	acc	gat	gaa	gag	cag	aag	ctg	787	
Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	Glu	Glu	Gln	Lys	Leu		
				215					220					225			
cgc	aac	gaa	tcc	cgc	aag	att	ctc	ggt	ctc	cca	gac	ctc	aag	gtc	tca	835	
Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	Asp	Leu	Lys	Val	Ser		
				230					235					240			245

ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att 883  
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile  
                   250                  255                  260

cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931  
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile  
                   265                  270                  275

ttg ggt gcc gct tca ggc gtc aag ctt gtc gac gtc cca acc cca ctt 979  
 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu  
                   280                  285                  290

gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac  
 1027  
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp  
                   295                  300                  305

tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac  
 1075  
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp  
                   310                  315                  320                  325

aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg  
 1123  
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu  
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 Leu Val Lys

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Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
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Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
                   50                  55                  60

Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
                   65                  70                  75                  80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn  
                   85                  90                  95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu  
                   100                  105                  110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn  
 115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His  
 130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val  
 145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala  
 165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala  
 180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val  
 195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp  
 210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro  
 225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly  
 245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp  
 260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp  
 275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly  
 290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu  
 305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile  
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Gln Ile Ala Glu Leu Leu Val Lys  
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 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser

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acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac			158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp			
15	20	25	30
cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc			206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val			
35	40	45	
acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc			254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr			
50	55	60	
gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt			302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val			
65	70	75	
ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac			350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn			
80	85	90	
aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca			398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala			
95	100	105	110
ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc			446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser			
115	120	125	
gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg			494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val			
130	135	140	
cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat			542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp			
145	150	155	
ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg			590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr			
160	165	170	
ctc ggc gct tcc atg gtt			608
Leu Gly Ala Ser Met Val			
175	180		

&lt;210&gt; 30

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 30

Met	Thr	Thr	Ala	Ser	Ala	Thr	Gly	Ile	Ala	Thr	Leu	Thr	Ser	Thr	Gly
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Asp	Val	Leu	Asp	Val	Trp	Tyr	Pro	Glu	Ile	Gly	Ser	Thr	Asp	Gln	Ser
	20						25						30		

Ala	Leu	Thr	Pro	Leu	Glu	Gly	Val	Asp	Glu	Asp	Arg	Asn	Val	Thr	Arg
	35						40					45			

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr  
 50 55 60  
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg  
 65 70 75 80  
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val  
 85 90 95  
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr  
 100 105 110  
 Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp  
 115 120 125  
 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile  
 130 135 140  
 Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr  
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 Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly  
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 Ala Ser Met Val  
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cttccatcat gttttaacta aggtttgtag gcttaaactc gtg aac tct gaa ctc 115  
 Val Asn Ser Glu Leu  
 1 5  
 aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163  
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg  
 10 15 20  
 ttg gta gat ata ccg agt ccg tcc ggt cag gaa aag cag att gct gat 211  
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp  
 25 30 35  
 gaa att gaa gat gcc ctt ccg aac ctt aat cta cct ggt gta gag gtc 259  
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val  
 40 45 50  
 ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc 307  
 Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala  
 55 60 65

tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
ttg gcc acg tcg act gag ctt aaa cat gat ctg acg ctg att gcg tat	499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
135 140 145	
gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag	595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160 165	
cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile	
170 175 180	
aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg	691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc	
1027	
Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val	
295 300 305	

ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt  
1075

Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg  
310 315 320 325

ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca  
1123

Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro  
330 335 340

agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg  
1171

Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr  
345 350 355

gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt  
1217

Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu  
360 365

cgggggttatc gtg  
1230

<210> 32

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Val Asn Ser Glu Leu Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile  
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Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu  
20 25 30

Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu  
35 40 45

Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr  
50 55 60

Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr  
65 70 75 80

Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met  
85 90 95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu  
100 105 110

His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu  
115 120 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly  
130 135 140

Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu  
145 150 155 160

Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln  
 165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser  
 180 185 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile  
 195 200 205

Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly  
 210 215 220

Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val  
 225 230 235 240

Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg  
 245 250 255

Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu  
 260 265 270

Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp  
 275 280 285

Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly  
 290 295 300

Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp  
 305 310 315 320

Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe  
 325 330 335

Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro  
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Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser  
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Glu

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 Met Ala Ser Ala Thr  
 1 5

ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc 163

Phe	Thr	Gly	Val	Ile	Pro	Pro	Val	Met	Thr	Pro	Leu	His	Ala	Asp	Gly	
				10					15					20		
agt	gtg	gat	gta	gaa	agc	ctc	cgc	aag	ctc	gtt	gac	cac	ctc	atc	aat	211
Ser	Val	Asp	Val	Glu	Ser	Leu	Arg	Lys	Leu	Val	Asp	His	Leu	Ile	Asn	
			25					30					35			
ggc	ggc	gtc	gac	gga	ctt	ttc	gca	ctg	ggc	tcc	tca	ggc	gaa	gcg	gca	259
Gly	Gly	Val	Asp	Gly	Leu	Phe	Ala	Leu	Gly	Ser	Ser	Gly	Glu	Ala	Ala	
		40					45					50				
ttc	ctc	acc	cgc	gcc	cag	cgc	aaa	ctc	gca	ctg	acc	acc	atc	atc	gag	307
Phe	Leu	Thr	Arg	Ala	Gln	Arg	Lys	Leu	Ala	Leu	Thr	Thr	Ile	Ile	Glu	
	55					60					65					
cac	acc	gca	ggc	cgc	gtt	ccc	gta	act	gct	ggc	gtc	att	gaa	acc	acc	355
His	Thr	Ala	Gly	Arg	Val	Pro	Val	Thr	Ala	Gly	Val	Ile	Glu	Thr	Thr	
	70				75					80					85	
act	gct	cgc	gtg	att	gag	ctc	gtg	gaa	gat	gcc	ctg	gag	gct	ggc	gcc	403
Thr	Ala	Arg	Val	Ile	Glu	Leu	Val	Glu	Asp	Ala	Leu	Glu	Ala	Gly	Ala	
				90				95						100		
gaa	ggc	ctc	gtt	gcc	act	gca	cct	ttc	tac	acc	cgc	acc	cac	gat	gtg	451
Glu	Gly	Leu	Val	Ala	Thr	Ala	Pro	Phe	Tyr	Thr	Arg	Thr	His	Asp	Val	
			105					110					115			
gaa	att	gaa	gaa	cac	ttc	cgc	aag	atc	cac	gcc	gcc	gct	cca	gag	ctt	499
Glu	Ile	Glu	Glu	His	Phe	Arg	Lys	Ile	His	Ala	Ala	Ala	Pro	Glu	Leu	
		120					125					130				
cca	ctg	ttt	gcc	tac	aac	atc	cca	gtg	tcg	gtg	cac	tcc	aac	ctc	aac	547
Pro	Leu	Phe	Ala	Tyr	Asn	Ile	Pro	Val	Ser	Val	His	Ser	Asn	Leu	Asn	
	135					140					145					
cca	gtc	atg	ctt	ttg	acg	ctg	gcc	aag	gat	ggc	gtt	ctt	gca	ggc	acc	595
Pro	Val	Met	Leu	Leu	Thr	Leu	Ala	Lys	Asp	Gly	Val	Leu	Ala	Gly	Thr	
	150				155				160					165		
aag	gat	tcc	agt	ggc	aat	gat	ggc	gca	atc	cgc	tca	ctg	atc	gaa	gct	643
Lys	Asp	Ser	Ser	Gly	Asn	Asp	Gly	Ala	Ile	Arg	Ser	Leu	Ile	Glu	Ala	
				170				175						180		
cgt	gat	gat	gct	gga	ctc	act	gag	cag	ttc	aag	atc	ctc	acc	ggc	agc	691
Arg	Asp	Asp	Ala	Gly	Leu	Thr	Glu	Gln	Phe	Lys	Ile	Leu	Thr	Gly	Ser	
			185					190					195			
gaa	acc	acc	gtt	gat	ttc	gcc	tac	ctt	gcg	ggc	gcc	gat	gga	gtt	gtc	739
Glu	Thr	Thr	Val	Asp	Phe	Ala	Tyr	Leu	Ala	Gly	Ala	Asp	Gly	Val	Val	
		200					205					210				
cca	ggc	ctg	ggc	aat	gtt	gat	cct	gca	gca	tac	gca	gct	tta	gca	aaa	787
Pro	Gly	Leu	Gly	Asn	Val	Asp	Pro	Ala	Ala	Tyr	Ala	Ala	Leu	Ala	Lys	
	215					220					225					
ctc	tgc	ctc	gat	gga	aag	tgg	gca	gaa	gct	gct	gct	ttg	cag	aag	cgc	835
Leu	Cys	Leu	Asp	Gly	Lys	Trp	Ala	Glu	Ala	Ala	Ala	Leu	Gln	Lys	Arg	
	230				235				240					245		
atc	aac	cac	ctc	ttc	cac	atc	gtc	ttc	gtg	gga	gac	acc	tcc	cat	atg	883
Ile	Asn	His	Leu	Phe	His	Ile	Val	Phe	Val	Gly	Asp	Thr	Ser	His	Met	

250 255 260

tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac 931  
Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His  
265 270 275

ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc 979  
Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu  
280 285 290

agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg  
1027  
Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu  
295 300 305

tac acc gct taaggccac acctcatgac tga  
1059  
Tyr Thr Ala  
310

<210> 34  
<211> 312  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 34  
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Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val  
20 25 30  
Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser  
35 40 45  
Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu  
50 55 60  
Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly  
65 70 75 80  
Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala  
85 90 95  
Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr  
100 105 110  
Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala  
115 120 125  
Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val  
130 135 140  
His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly  
145 150 155 160  
Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg  
165 170 175  
Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys

180	185	190
Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly		
195	200	205
Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr		
210	215	220
Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala		
225	230	235
Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly		
245	250	255
Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys		
260	265	270
Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val		
275	280	285
Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile		
290	295	300
Val Asp Glu Phe Leu Tyr Thr Ala		
305	310	

<210> 35  
 <211> 867  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(844)  
 <223> RXA00863

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 gtttgaaaaa ctcttcgccc cagcaaaatg aaggagcata atg gga atc aag gtt 115  
 Met Gly Ile Lys Val

	1	5	
ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca			163
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala			
10	15	20	
gtc aat gag tcc ga gat ctg gag ctt gtt gca gag atc ggc gtc gac			211
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp			
25	30	35	
gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac			259
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp			
40	45	50	
ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac			307
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn			
55	60	65	
aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt			355

Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg  
 70 75 80 85  
 ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403  
 Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val  
 90 95 100  
 ctg atc gca cct aac ttt gct atc tct gcg gtg ttg acc atg gtc ttt 451  
 Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe  
 105 110 115  
 tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg 499  
 Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu  
 120 125 130  
 cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act 547  
 His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr  
 135 140 145  
 gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag 595  
 Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln  
 150 155 160 165  
 cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta 643  
 Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val  
 170 175 180  
 gat gga atc ccg gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac 691  
 Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His  
 185 190 195  
 gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag 739  
 Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln  
 200 205 210  
 gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg 787  
 Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val  
 215 220 225  
 cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac 835  
 Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr  
 230 235 240 245  
 cta ggc ctg taaaggctca ttccagcagc ggg 867  
 Leu Gly Leu

&lt;210&gt; 36

&lt;211&gt; 248

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 36

Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln  
 1 5 10 15

Thr Ile Val Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala  
 20 25 30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala

35	40	45
Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu		
50	55	60
Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly		
65	70	75 80
Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys		
	85	90 95
Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val		
100	105	110
Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala		
115	120	125
Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly		
130	135	140
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala		
145	150	155 160
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser		
	165	170 175
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser		
	180	185 190
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr		
195	200	205
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly		
210	215	220
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val		
225	230	235 240
Gly Leu Glu His Tyr Leu Gly Leu		
	245	

<210> 37  
 <211> 873  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(850)  
 <223> RXA00864

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agcagcgggt ggaatttttt aaaaggagcg tttaaaggct gtg gcc gaa caa gtt 115  
 Val Ala Glu Gln Val  
 1 5

aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163  
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala

10	15	20	
gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag			211
Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu			
25	30	35	
ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga			259
Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg			
40	45	50	
act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac			307
Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His			
55	60	65	
act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att			355
Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile			
70	75	80	85
tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc			403
Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe			
90	95	100	
tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg			451
Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val			
105	110	115	
gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg			499
Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met			
120	125	130	
cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg			547
His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala			
135	140	145	
ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag			595
Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys			
150	155	160	165
cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc			643
Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser			
170	175	180	
aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc			691
Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly			
185	190	195	
atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta			739
Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val			
200	205	210	
gaa lgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat			787
Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp			
215	220	225	
ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg			835
Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro			
230	235	240	245
tat gtc atg gac ttt taacgcaaag ctcacaccca cga			873
Tyr Val Met Asp Phe			
250			

<210> 38  
 <211> 250  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 38  
 Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser  
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 Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
                     20                    25                    30  
 Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
                     35                    40                    45  
 Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
                     50                    55                    60  
 Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
     65                    70                    75                    80  
 Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
                     85                    90                    95  
 Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
                     100                    105                    110  
 Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu  
                     115                    120                    125  
 Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn  
     130                    135                    140  
 Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala  
     145                    150                    155                    160  
 Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro  
                     165                    170                    175  
 Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp  
                     180                    185                    190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile  
                     195                    200                    205  
 Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro  
     210                    215                    220  
 Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln  
     225                    230                    235                    240  
 Met Ala Thr Ser Pro Tyr Val Met Asp Phe  
                     245                    250

<210> 39  
 <211> 608  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (69)..(608)

&lt;223&gt; RXA02843

&lt;400&gt; 39

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tggacgtcatg	act	act	gct	tcc	gca	acc	gga	att	gca	aca	ctg	acc	tcc	110
	Met	Thr	Thr	Ala	Ser	Ala	Thr	Gly	Ile	Ala	Thr	Leu	Thr	Ser
1				5					10					

acc	ggc	gac	gtc	ctg	gac	gtg	tgg	tat	cca	gaa	atc	ggg	tcc	acc	gac	158
Thr	Gly	Asp	Val	Leu	Asp	Val	Trp	Tyr	Pro	Glu	Ile	Gly	Ser	Thr	Asp	
15				20					25					30		

cag	tcc	gcg	ctc	aca	cct	cta	gaa	ggc	gtc	gat	gaa	gat	cga	aac	gtc	206
Gln	Ser	Ala	Leu	Thr	Pro	Leu	Glu	Gly	Val	Asp	Glu	Asp	Arg	Asn	Val	
			35					40					45			

acc	cgc	aaa	atc	gtg	acg	aca	act	atc	gac	acc	gac	gca	gcc	ccc	acc	254
Thr	Arg	Lys	Ile	Val	Thr	Thr	Thr	Ile	Asp	Thr	Asp	Ala	Ala	Pro	Thr	
			50					55					60			

gac	acc	tac	gat	gca	tgg	ctg	cgc	ctt	cac	ctc	ctc	tcc	cac	cgc	gtt	302
Asp	Thr	Tyr	Asp	Ala	Trp	Leu	Arg	Leu	His	Leu	Leu	Ser	His	Arg	Val	
		65				70						75				

ttc	cgc	cct	cac	acc	atc	aac	cta	gac	ggc	att	ttc	ggc	ctc	ctc	aac	350
Phe	Arg	Pro	His	Thr	Ile	Asn	Leu	Asp	Gly	Ile	Phe	Gly	Leu	Leu	Asn	
	80					85					90					

aat	gtc	gtg	tgg	acc	aac	ttc	gga	cgc	tgc	gca	gtt	gac	ggt	ttc	gca	398
Asn	Val	Val	Trp	Thr	Asn	Phe	Gly	Pro	Cys	Ala	Val	Asp	Gly	Phe	Ala	
	95				100					105				110		

ctc	acc	cgc	gcg	cgc	ctg	tca	cgc	cga	ggc	caa	gtt	acg	gtt	tat	agc	446
Leu	Thr	Arg	Ala	Arg	Leu	Ser	Arg	Arg	Gly	Gln	Val	Thr	Val	Tyr	Ser	
			115						120					125		

gtc	gac	aag	ttc	cca	cgc	atg	gtc	gac	tat	gtg	gtt	ccc	tcg	ggc	gtg	494
Val	Asp	Lys	Phe	Pro	Arg	Met	Val	Asp	Tyr	Val	Val	Pro	Ser	Gly	Val	
		130						135					140			

cgc	atc	ggt	gac	gcc	gac	cgc	gtc	cga	ctt	ggc	gcg	tac	ctg	gca	gat	542
Arg	Ile	Gly	Asp	Ala	Asp	Arg	Val	Arg	Leu	Gly	Ala	Tyr	Leu	Ala	Asp	
		145					150					155				

ggc	acc	acc	gtg	atg	cat	gag	ggc	ttc	gtg	aac	ttc	aac	gct	ggc	acg	590
Gly	Thr	Thr	Val	Met	His	Glu	Gly	Phe	Val	Asn	Phe	Asn	Ala	Gly	Thr	
	160					165					170					

ctc	ggc	gct	tcc	atg	gtt											608
Leu	Gly	Ala	Ser	Met	Val											
175					180											

&lt;210&gt; 40

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 40

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Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
 1              5              10              15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
      20              25              30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
      35              40              45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
      50              55              60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
      65              70              75              80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
      85              90              95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
      100             105             110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
      115             120             125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
      130             135             140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
      145             150             155             160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
      165             170             175

Ala Ser Met Val
      180

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&lt;210&gt; 41

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1120)

&lt;223&gt; RXN00355

&lt;400&gt; 41

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aatagatcag cgcacccgtg gtggaaccaa aaggctcaac aatacgaaac gttcgttttc 60

ggtcctgatg aaagagatgt cctgaaatca tcatctaagt atg cat ctc ggt aag      115
                               Met His Leu Gly Lys
                               1              5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg      163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
      10              15              20

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acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc	211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser	
25 30 35	
gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc	259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile	
40 45 50	
ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc	307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val	
55 60 65	
gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc	355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys	
70 75 80 85	
atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag	403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln	
90 95 100	
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc	451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg	
105 110 115	
cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca	499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala	
120 125 130	
ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc	547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val	
135 140 145	
tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc	595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly	
150 155 160 165	
cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc	643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly	
170 175 180	
gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa	691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu	
185 190 195	
aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac	739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His	
200 205 210	
aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc	787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile	
215 220 225	
gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc	835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val	
230 235 240 245	
gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc	883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly	
250 255 260	
atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc	931

Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe  
 265 270 275

aac cac acc gtg gaa tac atc ctc aag ctg gac cga aac cca gat ttc 979  
 Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp Arg Asn Pro Asp Phe  
 280 285 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag  
 1027

Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys  
 295 300 305

cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac  
 1075

Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr  
 310 315 320 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc  
 1120

Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val  
 330 335 340

taatttagct cgaggggcaa gga  
 1143

<210> 42  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 42  
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Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
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Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
 35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
 50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
 65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
 85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
 100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
 115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe  
 130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln  
 145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu  
 165 170 175  
 Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser  
 180 185 190  
 Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr  
 195 200 205  
 Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala  
 210 215 220  
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe  
 225 230 235 240  
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp  
 245 250 255  
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly  
 260 265 270  
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp  
 275 280 285  
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala  
 290 295 300  
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu  
 305 310 315 320  
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile  
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 Ala Arg Asp Val  
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&lt;210&gt; 43

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(958)

&lt;223&gt; FRXA00352

&lt;400&gt; 43

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ggtcctgatg aaagagatgt cccatgaatca tcacttaagt atg cat ctc ggt aag 115  
 Met His Leu Gly Lys  
 1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163  
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met  
 10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211  
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser

25	30	35	
gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile 40 45 50			259
ttc tgc cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val 55 60 65			307
gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys 70 75 80 85			355
atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln 90 95 100			403
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg 105 110 115			451
cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala 120 125 130			499
ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val 135 140 145			547
tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly 150 155 160 165			595
cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly 170 175 180			643
gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu 185 190 195			691
aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His 200 205 210			739
aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile 215 220 225			787
gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val 230 235 240 245			835
gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly 250 255 260			883
atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe 265 270 275			931

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           280                          285

958

<210> 44  
 <211> 286  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 44  
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 Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
                           20                          25                          30  
 Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
                           35                          40                          45  
 Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
                           50                          55                          60  
 Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
   65                          70                          75                          80  
 Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
                           85                          90                          95  
 Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
                           100                          105                          110  
 Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
                           115                          120                          125  
 Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe  
   130                          135                          140  
 Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln  
   145                          150                          155                          160  
 His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu  
                           165                          170                          175  
 Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser  
                           180                          185                          190  
 Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr  
                           195                          200                          205  
 Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala  
                           210                          215                          220  
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe  
   225                          230                          235                          240  
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp  
                           245                          250                          255  
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly

260 265 270  
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 275 280 285

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<220>  
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 <222> (1)..(1377)  
 <223> RXA00972

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 Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn  
 20 25 30  
 gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg 144  
 Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu  
 35 40 45  
 cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag 192  
 Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu  
 50 55 60  
 gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga 240  
 Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly  
 65 70 75 80  
 cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att 288  
 Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile  
 85 90 95  
 gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc 336  
 Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile  
 100 105 110  
 aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc 384  
 Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile  
 115 120 125  
 acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt 432  
 Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val  
 130 135 140  
 caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa 480  
 Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu  
 145 150 155 160  
 ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg 528  
 Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu  
 165 170 175

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc 576  
 Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala  
 180 185 190

act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc 624  
 Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser  
 195 200 205

gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg 672  
 Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu  
 210 215 220

gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc 720  
 Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly  
 225 230 235 240

ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac 768  
 Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His  
 245 250 255

agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac 816  
 Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr  
 260 265 270

ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt 864  
 Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val  
 275 280 285

gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc 912  
 Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly  
 290 295 300

atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc 960  
 Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly  
 305 310 315 320

ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac  
 1008  
 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His  
 325 330 335

gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg  
 1056  
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 340 345 350

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 1104  
 Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg  
 355 360 365

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 1152  
 Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val  
 370 375 380

ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac  
 1200  
 Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr  
 385 390 395 400

cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc  
1248

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly  
405 410 415

gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc  
1296

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro  
420 425 430

gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc  
1344

Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg  
435 440 445

gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga  
1397

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1400

<210> 46

<211> 459

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

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35 40 45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu  
50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly  
65 70 75 80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile  
85 90 95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile  
100 105 110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile  
115 120 125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val  
130 135 140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu  
145 150 155 160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu

165										170					175				
Ile	Arg	Val	Lys	Pro	Gly	Ile	Glu	Ala	His	Thr	His	Glu	Phe	Ile	Ala				
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Thr	Ser	His	Glu	Asp	Gln	Lys	Phe	Gly	Phe	Ser	Leu	Ala	Ser	Gly	Ser				
			195					200					205						
Ala	Phe	Glu	Ala	Ala	Lys	Ala	Ala	Asn	Asn	Ala	Glu	Asn	Leu	Asn	Leu				
			210				215					220							
Val	Gly	Leu	His	Cys	His	Val	Gly	Ser	Gln	Val	Phe	Asp	Ala	Glu	Gly				
			225				230				235				240				
Phe	Lys	Leu	Ala	Ala	Glu	Arg	Val	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	His				
				245					250					255					
Ser	Glu	Leu	Gly	Val	Ala	Leu	Pro	Glu	Leu	Asp	Leu	Gly	Gly	Gly	Tyr				
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Gly	Ile	Ala	Tyr	Thr	Ala	Ala	Glu	Glu	Pro	Leu	Asn	Val	Ala	Glu	Val				
			275					280				285							
Ala	Ser	Asp	Leu	Leu	Thr	Ala	Val	Gly	Lys	Met	Ala	Ala	Glu	Leu	Gly				
			290				295				300								
Ile	Asp	Ala	Pro	Thr	Val	Leu	Val	Glu	Pro	Gly	Arg	Ala	Ile	Ala	Gly				
			305				310				315				320				
Pro	Ser	Thr	Val	Thr	Ile	Tyr	Glu	Val	Gly	Thr	Thr	Lys	Asp	Val	His				
				325					330					335					
Val	Asp	Asp	Asp	Lys	Thr	Arg	Arg	Tyr	Ile	Ala	Val	Asp	Gly	Gly	Met				
			340					345					350						
Ser	Asp	Asn	Ile	Arg	Pro	Ala	Leu	Tyr	Gly	Ser	Glu	Tyr	Asp	Ala	Arg				
			355				360					365							
Val	Val	Ser	Arg	Phe	Ala	Glu	Gly	Asp	Pro	Val	Ser	Thr	Arg	Ile	Val				
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Gly	Ser	His	Cys	Glu	Ser	Gly	Asp	Ile	Leu	Ile	Asn	Asp	Glu	Ile	Tyr				
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Pro	Ser	Asp	Ile	Thr	Ser	Gly	Asp	Phe	Leu	Ala	Leu	Ala	Ala	Thr	Gly				
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Ala	Tyr	Cys	Tyr	Ala	Met	Ser	Ser	Arg	Tyr	Asn	Ala	Phe	Thr	Arg	Pro				
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Ala	Val	Val	Ser	Val	Arg	Ala	Gly	Ser	Ser	Arg	Leu	Met	Leu	Arg	Arg				
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Glu	Thr	Leu	Asp	Asp	Ile	Leu	Ser	Leu	Glu	Ala									
			450				455												

&lt;210&gt; 47

&lt;211&gt; 2121

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2098)

&lt;223&gt; RXA02653

&lt;400&gt; 47

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                                         Met Ile Pro Lys Pro
                                         1 5

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Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Asn Glu Gly Ser Glu
                        10 15 20

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Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys
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gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa 259
Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu
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Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu
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Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His
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Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu
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Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Gly Val Val Pro
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Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg
                        150 155 160 165

cct ggg act cgg ggg tta gat gta gcg gct gac ggc acc gtt caa ggg 643
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly
                        170 175 180

caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg 691
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu
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gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat 787  
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 215 220 225

ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc 835  
 Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu  
 230 235 240 245

act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt 883  
 Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser  
 250 255 260

cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag 931  
 Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu  
 265 270 275

ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt 979  
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 280 285 290

gcc cgc aaa gcg aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac  
 1027  
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 295 300 305

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 1075  
 Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val  
 310 315 320 325

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 1219  
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 375 380 385

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 1363

Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His  
410 415 420

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1411

Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu Ala Leu Gln Glu Cys  
425 430 435

tgc caa ctc gtc gat tct ctc aga gaa tgc ggg cat tcc cca cag ttt  
1459

Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe  
440 445 450

att gac ctt gga gga ggg gtg cct atg agc tac att gaa tct gag gaa  
1507

Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu  
455 460 465

gat tgg atc cgt tat caa tcc gct aaa tct gcg act tca gcc ggg tat  
1555

Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr  
470 475 480 485

gcc gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg  
1603

Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro  
490 495 500

ttc tat cag acc cca gtg cgc ggt aat tgg ttg aaa gac gtg ctt tct  
1651

Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser  
505 510 515

aag ggg gta gct cag atg ctc att gac cgg gga ttg cgg tta cac ata  
1699

Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile  
520 525 530

gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa  
1747

Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu  
535 540 545

gtt gct ttt gtg aaa acc cga agt gac ggg ttg cct cta gtg gga ctg  
1795

Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu  
550 555 560 565

gct atg aac cga acg cag tgc cgg act aca tcc gat gat ttt ctc att  
1843

Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile  
570 575 580

gat ccc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gca  
1891

Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala  
585 590 595

tat cta gtg ggt gcc tac tgc atc gaa gat gag ctg att tta cgc cgg  
1939

Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg

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        600                605                610

cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att
1987
Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile
  615                620                625

cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac
2035
Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His
  630                635                640                645

caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac
2083
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
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2121
Asp Ile Asp Ala Asp
      665

<210> 48
<211> 666
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
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Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu
      20         25         30

Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly
      35         40         45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
      50         55         60

Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
      65         70         75         80

Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro
      85         90         95

Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val
      100        105        110

Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu
      115        120        125

Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro
      130        135        140

Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly
      145        150        155        160

Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp
      165        170        175

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Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr  
 180 185 190  
 Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp  
 195 200 205  
 Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr  
 210 215 220  
 Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro  
 225 230 235 240  
 Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile  
 245 250 255  
 Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro  
 260 265 270  
 Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp  
 275 280 285  
 Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val  
 290 295 300  
 Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg  
 305 310 315 320  
 Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile  
 325 330 335  
 Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu  
 340 345 350  
 Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile  
 355 360 365  
 Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala  
 370 375 380  
 Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala  
 385 390 395 400

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Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val  
 405 410 415  
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu  
 420 425 430  
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly  
 435 440 445  
 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr  
 450 455 460  
 Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala  
 465 470 475 480  
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu  
 485 490 495

Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu  
 500 505 510  
 Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly  
 515 520 525  
 Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly  
 530 535 540  
 Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu  
 545 550 555 560  
 Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser  
 565 570 575  
 Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly  
 580 585 590  
 Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu  
 595 600 605  
 Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly  
 610 615 620  
 Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu  
 625 630 635 640  
 Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro  
 645 650 655  
 Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp  
 660 665

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA01393

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 agtaaaatga ttggttctta acatgggtta atatagcttc atg aac ccc att caa 115  
 Met Asn Pro Ile Gln  
 1 5  
 ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163  
 Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala  
 10 15 20  
 tcc tta gcc ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa 211  
 Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys  
 25 30 35  
 gct ctc gag cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg 259  
 Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro

40	45	50	
gcc aaa gca acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa			307
Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys			
55	60	65	
atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt			355
Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu			
70	75	80	85
gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca			403
Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr			
	90	95	100
tgg ttt cct ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg			451
Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr			
	105	110	115
ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg			499
Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg			
	120	125	130
cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg			547
Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala			
135	140	145	
gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca			595
Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala			
150	155	160	165
acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg			643
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp			
	170	175	180
gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac			691
Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp			
	185	190	195
cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta			739
Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Val			
200	205	210	
ctc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc			787
Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly			
215	220	225	
ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa			835
Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys			
230	235	240	245
gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg			883
Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met			
	250	255	260
tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca			931
Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr			
	265	270	275
gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc			980
Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu Arg Pro			
280	285	290	

tgaaaagggtt cag

993

&lt;210&gt; 50

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 50

Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly  
 1 5 10 15

Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val  
 20 25 30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val  
 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val  
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln  
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala  
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser  
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr  
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu  
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg  
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp  
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys  
 180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val  
 195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu  
 210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala  
 225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro  
 245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser  
 260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu  
 275 280 285

Arg Pro  
 290

<210> 51  
 <211> 1626  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1603)  
 <223> RXA00241

<400> 51  
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aagtttagcg acttcgccgt acgtcaacta cggttaaata gtg aat act caa tca 115  
 Val Asn Thr Gln Ser  
 1 5

gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct 163  
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser  
 10 15 20

att aga acc ctc atc gcg ctg atc atc gga tcg acc gtc ggc gcg gga 211  
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly  
 25 30 35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259  
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala  
 40 45 50

atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307  
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala  
 55 60 65

ttc gtg ttc cat gtt ctt gcc cgc cgt aaa cct cac ctc gat tct ggc 355  
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly  
 70 75 80 85

gtc tac gca tat gcg cgt gtt gga ttg ggc gat tat gta ggt ttc tcc 403  
 Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser  
 90 95 100

tcc gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac 451  
 Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr  
 105 110 115

gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc 499  
 Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser  
 120 125 130

caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg 547  
 Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp  
 135 140 145

ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg 595

Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu  
 150 155 160 165  
 aca acg gtc acc acc gtg gcc aaa att ctg cct ctg ttg tgc ttc atc 643  
 Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile  
 170 175 180  
 atc ctt gtt gca ttc ttg gcc ttt agc tgg gag aag ttc act gtt gat 691  
 Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp  
 185 190 195  
 tta tgg gcg cgt gat ggt gcc gtg gcc agc att ttt gat cag gtg cgc 739  
 Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg  
 200 205 210  
 gcc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca 787  
 Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala  
 215 220 225  
 tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct 835  
 Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala  
 230 235 240 245  
 acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct 883  
 Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser  
 250 255 260  
 tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca 931  
 Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro  
 265 270 275  
 gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt 979  
 Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly  
 280 285 290  
 gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat  
 1027  
 Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr  
 295 300 305  
 gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg  
 1075  
 Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met  
 310 315 320 325  
 gat gcc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct  
 1123  
 Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala  
 330 335 340  
 gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc  
 1171  
 Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile  
 345 350 355  
 atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg  
 1219  
 Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu  
 360 365 370

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg  
1267

Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu  
375 380 385

gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc  
1315

Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly  
390 395 400 405

aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc  
1363

Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg  
410 415 420

aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg  
1411

Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu  
425 430 435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg  
1459

Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met  
440 445 450

ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa  
1507

Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu  
455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt  
1555

Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val  
470 475 480 485

gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt  
1603

Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu  
490 495 500

taaacaccga aaccttctg cta  
1626

<210> 52

<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr  
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Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser  
20 25 30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val  
35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly  
50 55 60

Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro  
 65 70 75 80  
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp  
 85 90 95  
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile  
 100 105 110  
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr  
 115 120 125  
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val  
 130 135 140  
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser  
 145 150 155 160  
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro  
 165 170 175  
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu  
 180 185 190  
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile  
 195 200 205  
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile  
 210 215 220  
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser  
 225 230 235 240  
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu  
 245 250 255  
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu  
 260 265 270  
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val  
 275 280 285  
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser  
 290 295 300  
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu  
 305 310 315 320  
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile  
 325 330 335  
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val  
 340 345 350  
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val  
 355 360 365  
 Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe  
 370 375 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr  
 385 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser  
 405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val  
 420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe  
 435 440 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg  
 450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val  
 465 470 475 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn  
 485 490 495

Gly Ser Leu Ser Leu  
 500

<210> 53  
 <211> 822  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(799)  
 <223> RXA01394

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 tcatttttact taagtacttc cataggtcac gatgggtgatc atg gaa atc ttc att 115  
 Met Glu Ile Phe Ile  
 1 5

aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag 163  
 Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Ser Ile Gly Pro Gln  
 10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211  
 Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala  
 25 30 35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc 259  
 Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly  
 40 45 50

acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat 307  
 Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp  
 55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355  
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met  
 70 75 80 85

gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att 403  
 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile  
                   90                                  95                                  100

gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg ggc ggt tcg 451  
 Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser  
                   105                                  110                                  115

gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc 499  
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val  
                   120                                  125                                  130

gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg 547  
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu  
                   135                                  140                                  145

acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc ggc 595  
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly  
                   150                                  155                                  160                                  165

ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct 643  
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala  
                   170                                  175                                  180

ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc 691  
 Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly  
                   185                                  190                                  195

gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg 739  
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp  
                   200                                  205                                  210

atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg 787  
 Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu  
                   215                                  220                                  225

atg ttg atg ggt tagttttcgc gggttttgga atc 822  
 Met Leu Met Gly  
 230

&lt;210&gt; 54

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 54

Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu  
   1                                  5                                  10                                  15

Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg  
                   20                                  25                                  30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe  
                   35                                  40                                  45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala  
                   50                                  55                                  60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu

65	70	75	80
Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu	85	90	95
Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr	100	105	110
Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg	115	120	125
Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu	130	135	140
Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala	145	150	155
Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg	165	170	175
Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro	180	185	190
Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro	195	200	205
Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala	210	215	220
Leu Ala Ile Lys Leu Met Leu Met Gly	225	230	

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 <223> EXA00865

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 Met Ser Thr Gly Leu  
 1 5  
  
 aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163  
 Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met  
 10 15 20  
  
 gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211  
 Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg  
 25 30 35  
  
 gaa gtc gcg gct tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc 259  
 Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu  
 40 45 50

gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta	307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
55 60 65	
gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc	355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
gaa gct gct gct tct gct ggc gca gac ggc ctt tta gtt gta act cct	451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
105 110 115	
tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca	499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala	
120 125 130	
att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt	547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly	
135 140 145	
cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa	595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
150 155 160 165	
tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca	643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
170 175 180	
gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat	691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
185 190 195	
gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att	739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
200 205 210	
tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca	787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa	835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
230 235 240 245	
cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg	883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
250 255 260	
gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga	931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
265 270 275	
ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa	979
Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu	
280 285 290	

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1026

Asp Met Lys Lys Ala Gly Val Leu

295

300

<210> 56

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr

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10

15

Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp

20

25

30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu

35

40

45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr

50

55

60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly

65

70

75

80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr

85

90

95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu

100

105

110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu

115

120

125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu

130

135

140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met

145

150

155

160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys

165

170

175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala

180

185

190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly

195

200

205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu

210

215

220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg

225

230

235

240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu

245

250

255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn

260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu  
275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  
290 295 300

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<213> Corynebacterium glutamicum

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<223> RXS02021

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Met Ser Glu Asn Ile  
1 5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163  
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr  
10 15 20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211  
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln  
25 30 35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca 259  
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala  
40 45 50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307  
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp  
55 60 65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct 355  
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser  
70 75 80 85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt 403  
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu  
90 95 100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451  
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu  
105 110 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499  
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro  
120 125 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc 547  
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile  
135 140 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595  
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val  
 150 155 160 165  
  
 ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643  
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala  
 170 175 180  
  
 tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691  
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe  
 185 190 195  
  
 aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739  
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser  
 200 205 210  
  
 ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787  
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile  
 215 220 225  
  
 cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835  
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly  
 230 235 240 245  
  
 caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883  
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu  
 250 255 260  
  
 gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931  
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr  
 265 270 275  
  
 ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979  
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile  
 280 285 290  
  
 gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag  
 1027  
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu  
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cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc  
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 Pro Val Ala Arg Leu Lys Ala  
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<210> 58  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 58  
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 Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

35	40	45
Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val 50 55 60		
Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val 65 70 75 80		
Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu 85 90 95		
Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His 100 105 110		
Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys 115 120 125		
Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg 130 135 140		
Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met 145 150 155 160		
Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg 165 170 175		
Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu 180 185 190		
Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu 195 200 205		
Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly 210 215 220		
Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu 225 230 235 240		
Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile 245 250 255		
Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val 260 265 270		
Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg 275 280 285		
Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu 290 295 300		
Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala 305 310 315		

&lt;210&gt; 59

&lt;211&gt; 1296

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1273)

&lt;223&gt; RXS02157

&lt;400&gt; 59

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caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115  
 Met Ser Thr Leu Glu  
 1 5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163  
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu  
 10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211  
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val  
 25 30 35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259  
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala  
 40 45 50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307  
 His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly  
 55 60 65

cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355  
 His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu  
 70 75 80 85

gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403  
 Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln  
 90 95 100

acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451  
 Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala  
 105 110 115

ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499  
 Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val  
 120 125 130

cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547  
 His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln  
 135 140 145

cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595  
 Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe  
 150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643  
 Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn  
 170 175 180

cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg 691  
 Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr  
 185 190 195

ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg 739  
 Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu  
 200 205 210

tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787  
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly  
 215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835  
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val  
 230 235 240 245

ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883  
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile  
 250 255 260

ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931  
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly  
 265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979  
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala  
 280 285 290

aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc  
 1027  
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala  
 295 300 305

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt  
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 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330 335 340

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 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg  
 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
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 375 380 385

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 Ile Ala  
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<210> 60

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

&lt;400&gt; 60

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           20           25           30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
           35           40           45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50           55           60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65           70           75           80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
           85           90           95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
          100          105          110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
          115          120          125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
          130          135          140

Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
          145          150          155          160

Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
          165          170          175

Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
          180          185          190

Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
          195          200          205

Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
          210          215          220

Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
          225          230          235          240

His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
          245          250          255

Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
          260          265          270

Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
          275          280          285

Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
          290          295          300

Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
          305          310          315          320

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 Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu  
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atc ggt agc ctg ttg tct ttg ttc cag gcg cgg atg ctc aac cgc atc 547  
 Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile  
 135 140 145

gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc 595  
 Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile  
 150 155 160 165

cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg 643  
 His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu  
 170 175 180

ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa 691  
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 185 190 195

caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg 739  
 Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val  
 200 205 210

ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg 787  
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 215 220 225

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt 835  
 Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg  
 230 235 240 245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat 883  
 Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn  
 250 255 260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc 931  
 Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe  
 265 270 275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct 979  
 Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala  
 280 285 290

tgt gta taaggccagc tttggtgccc agt  
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 Cys Val  
 295

<210> 62  
 <211> 295  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 62  
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 1 5 10 15  
 Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu

20					25					30						
Phe	Gly	Ile	Leu	Gly	His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe	
35					40					45						
Leu	Ala	Val	Leu	Ser	Val	Gly	Leu	Thr	Val	Leu	Gly	Pro	Trp	Leu	Leu	
50					55					60						
Gly	Lys	Ala	Thr	Asn	Val	Val	Phe	Glu	Gly	Phe	Leu	Ser	Lys	Arg	Met	
65					70					75					80	
Pro	Ala	Gly	Ala	Ser	Lys	Glu	Asp	Ile	Ile	Ala	Gln	Leu	Gln	Ala	Ala	
85					90					95						
Gly	Lys	His	Asn	Gln	Ala	Ser	Met	Met	Glu	Asp	Met	Asn	Leu	Val	Pro	
100					105					110						
Gly	Ser	Gly	Ile	Asp	Phe	Glu	Lys	Leu	Ala	Met	Ile	Leu	Gly	Leu	Val	
115					120					125						
Ile	Gly	Ala	Tyr	Leu	Ile	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Gln	Ala	Arg	
130					135					140						
Met	Leu	Asn	Arg	Ile	Val	Gln	Ser	Ala	Met	His	Arg	Leu	Arg	Met	Glu	
145					150					155					160	
Val	Glu	Glu	Lys	Ile	His	Arg	Leu	Pro	Leu	Ser	Tyr	Phe	Asp	Ser	Ile	
165					170					175						
Lys	Arg	Gly	Asp	Leu	Leu	Ser	Arg	Val	Thr	Asn	Asp	Val	Asp	Asn	Ile	
180					185					190						
Gly	Gln	Ser	Leu	Gln	Gln	Thr	Leu	Ser	Gln	Ala	Ile	Thr	Ser	Leu	Leu	
195					200					205						
Thr	Val	Ile	Gly	Val	Leu	Val	Met	Met	Phe	Ile	Ile	Ser	Pro	Leu	Leu	
210					215					220						
Ala	Leu	Val	Ala	Leu	Val	Ser	Ile	Pro	Val	Thr	Ile	Val	Val	Thr	Val	
225					230					235					240	
Val	Val	Ala	Ser	Arg	Ser	Gln	Lys	Leu	Phe	Ala	Glu	Gln	Trp	Lys	Gln	
245					250					255						
Thr	Gly	Ile	Leu	Asn	Ala	Arg	Leu	Glu	Glu	Thr	Tyr	Ser	Gly	His	Ala	
260					265					270						
Val	Val	Lys	Val	Phe	Gly	His	Gln	Lys	Asp	Val	Gln	Glu	Ala	Phe	Glu	
275					280					285						
Glu	Glu	Asn	Gln	Ala	Cys	Val										
290					295											

&lt;210&gt; 63

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(426)

&lt;223&gt; RXC00861

&lt;400&gt; 63

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atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag      48
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
   1             5             10             15

cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc      96
Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20             25             30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca     144
Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
             35             40             45

ggg aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc     192
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
   50             55             60

ggg gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc     240
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
   65             70             75             80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg     288
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
             85             90             95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac     336
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
             100             105             110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt     384
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
             115             120             125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca            426
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
             130             135             140

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&lt;210&gt; 64

&lt;211&gt; 142

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 64

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Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
   1             5             10             15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
             20             25             30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
             35             40             45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
   50             55             60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
   65             70             75             80

```

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro  
85 90 95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn  
100 105 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu  
115 120 125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala  
130 135 140

<210> 65

<211> 1066

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1066)

<223> RXC00866

<400> 65

gcatcaacgt aggagatcct cgacttccaa ttatggctcc aaatgagcag gaacttgagg 60

ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115  
Met Asn Asp Ser Arg  
1 5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt 163  
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly  
10 15 20

cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc 211  
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser  
25 30 35

tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg 259  
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg  
40 45 50

gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307  
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln  
55 60 65

aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355  
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn  
70 75 80 85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403  
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly  
90 95 100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451  
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln  
105 110 115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499  
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys

120	125	130	
tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag			547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys			
135	140	145	
gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa			595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu			
150	155	160	165
atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc			643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile			
	170	175	180
gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac			691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp			
	185	190	195
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc			739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val			
	200	205	210
gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att			787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile			
	215	220	225
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt			835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg			
	230	235	240
ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt			883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg			
	250	255	260
ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg			931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro			
	265	270	275
ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt			979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu			
	280	285	290
ggc ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac			
1027			
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp			
	295	300	305
atc aag ctg gat cag act cct cct gat gga cgc cca act			
1066			
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr			
	310	315	320
<210> 66			
<211> 322			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 66			
Met Asn Asp Ser Arg Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly			
	1	5	10
			15

Pro Pro Glu Ala Gly Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln  
                     20                    25                    30  
 Ala Pro Asp Ala Ser Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala  
                     35                    40                    45  
 Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp  
                     50                    55                    60  
 Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly  
                     65                    70                    75                    80  
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly  
                     85                    90                    95  
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly  
                     100                    105                    110  
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg  
                     115                    120                    125  
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu  
                     130                    135                    140  
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu  
                     145                    150                    155                    160  
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn  
                     165                    170                    175  
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly  
                     180                    185                    190  
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp  
                     195                    200                    205  
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp  
                     210                    215                    220  
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro  
                     225                    230                    235                    240  
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys  
                     245                    250                    255  
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn  
                     260                    265                    270  
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser  
                     275                    280                    285  
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val  
                     290                    295                    300  
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg  
                     305                    310                    315                    320  
 Pro Thr

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<220>
<221> CDS
<222> (101)..(1504)
<223> RXC02095
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ctt	cgc	tat	gcc	agt	caa	ttt	gga	cgg	cga	tac	acc	gca	ggc	aag	ctc	451
Leu	Arg	Tyr	Ala	Ser	Gln	Phe	Gly	Arg	Arg	Tyr	Thr	Ala	Gly	Lys	Leu	
			105					110					115			
agc	atg	ggg	gta	cag	cat	gat	gtc	cgg	ctt	aaa	acg	atg	cgc	tca	ttg	499
Ser	Met	Gly	Val	Gln	His	Asp	Val	Arg	Leu	Lys	Thr	Met	Arg	Ser	Leu	
		120					125					130				
cag	aac	ctc	gat	ggg	cca	ggg	cag	gac	tct	att	cgc	aca	ggc	caa	gta	547
Gln	Asn	Leu	Asp	Gly	Pro	Gly	Gln	Asp	Ser	Ile	Arg	Thr	Gly	Gln	Val	
		135				140					145					
gtc	agt	cgg	tcc	att	tcg	gat	atc	aac	atg	gtg	caa	agc	ctt	gtg	gcg	595
Val	Ser	Arg	Ser	Ile	Ser	Asp	Ile	Asn	Met	Val	Gln	Ser	Leu	Val	Ala	
150					155					160					165	
atg	ttg	ccg	atg	ttg	atc	gga	aat	gtg	gtc	aag	ctt	gtg	ctc	act	ttg	643
Met	Leu	Pro	Met	Leu	Ile	Gly	Asn	Val	Val	Lys	Leu	Val	Leu	Thr	Leu	
				170					175				180			

gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg 691  
 Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val  
 185 190 195

ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt 739  
 Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu  
 200 205 210

ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act 787  
 Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr  
 215 220 225

cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg 835  
 His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala  
 230 235 240 245

cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta 883  
 Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu  
 250 255 260

ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc 931  
 Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro  
 265 270 275

atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt gcc 979  
 Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly  
 280 285 290

ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg  
 1027  
 Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val  
 295 300 305

gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg  
 1075  
 Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu  
 310 315 320 325

tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc  
 1123  
 Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg  
 330 335 340

atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac  
 1171  
 Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His  
 345 350 355

ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta  
 1219  
 Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val  
 360 365 370

gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt  
 1267  
 Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly  
 375 380 385

gaa acc gtt gtg ttg gtg gcc cct cca ggt tca ggc aag acc atg gct  
 1315

Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala  
390 395 400 405

gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc  
1363

Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala  
410 415 420

ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc  
1411

Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser  
425 430 435

gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac  
1459

Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr  
440 445 450

tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag  
1504

Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln  
455 460 465

tgatgagcag atcgaacacg cag  
1527

<210> 68

<211> 468

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala  
1 5 10 15

Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln  
20 25 30

Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr  
35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile  
50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg  
65 70 75 80

Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile  
85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr  
100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys  
115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile  
130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val

145                      150                      155                      160  
 Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys  
                          165                      170                      175  
 Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr  
                          180                      185                      190  
 Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr  
                          195                      200                      205  
 Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala  
                          210                      215                      220  
 Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val  
 225     230     235     240  
 Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu  
    245     250     255  
 Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr  
    260     265     270  
 Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val  
    275     280     285  
 Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr  
    290     295     300  
 Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala  
 305     310     315     320  
 Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu  
    325     330     335  
 Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg  
    340     345     350  
 Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu  
    355     360     365  
 Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu  
    370     375     380  
 Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser  
 385     390     395     400  
 Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp  
    405     410     415  
 Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp  
    420     425     430  
 Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp  
    435     440     445  
 Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly  
    450     455     460  
 Phe Gly Cys Gln  
 465

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<220>
<221> CDS
<222> (84) .. (272)
<223> RXC03185
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<400> 69
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tcaactgagct gtccgaaacc accatg aat gat ctt gca gct gaa ggt gaa aac 113
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
30 35 40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
45 50 55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
Ser Arg Glu Ser Leu
60

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<210> 70
<211> 63
<212> PRT
<213> Corynebacterium glutamicum
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<400> 70
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
 1              5              10              15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
      20              25              30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
      35              40              45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
      50              55              60

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<210> 71
<211> 4653
<212> DNA
<213> Corynebacterium glutamicum
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&lt;221&gt; CDS

&lt;222&gt; (101)..(4630)

&lt;223&gt; RXN00367

&lt;400&gt; 71

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atcgaaagta acccttttgt tacttgcgtt gcaggtagtg tccctgattt tcttattatc 60

gaacgattga tagaaacagg attaaagtga ggtatcccgc atg aaa cca caa gga 115
                                         Met Lys Pro Gln Gly
                                         1           5

ctc tac aac cct gcg cat gaa cat gac gcc tgc ggt gtg gcg ttt att 163
Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys Gly Val Ala Phe Ile
                        10                        15                        20

gcg gat atc cac ggt cga ccc agc cgc agc att gtt gat cgt gca ctt 211
Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile Val Asp Arg Ala Leu
                        25                        30                        35

gag gcg ctt cgc aac att gac cac cga ggt gcc gcc ggt gca gag aag 259
Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala Ala Gly Ala Glu Lys
                        40                        45                        50

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307
Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe
                        55                        60                        65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc 355
Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala
                        70                        75                        80                        85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct 403
Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala
                        90                        95                        100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt 451
Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu
                        105                        110                        115

ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct 499
Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala
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gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga 547
Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly
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aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt 595
Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg
                        150                        155                        160                        165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc 643
Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe
                        170                        175                        180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act 69..
Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr
                        185                        190                        195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag 739
Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu

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200	205	210	
tcg gcc att gct att gtg cac	tcg cgt ttc tcc acg aac act ttc cca		787
Ser Ala Ile Ala Ile Val His	Ser Arg Phe Ser Thr Asn Thr Phe Pro		
215	220	225	
agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag			835
Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu			
230	235	240	245
atc aac act gtg cgt ggc aat gaa aac tgg atg cgc gcc cgc gag gcg			883
Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala			
	250	255	260
ctt atc aaa aac gac aag ctg ggc aat ttg agc agc gtg ctg cct atc			931
Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile			
	265	270	275
tgc acc ccg gag ggc tgc gat acc gcg cgt ttc gac gag gct ttg gag			979
Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu			
	280	285	290
ctt ttg cac ctg ggc gga tac tca ctt ccg cat gct gtt gcg atg atg			
1027			
Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His Ala Val Ala Met Met			
	295	300	305
atc cct cag gcg tgg gaa cac aac aag acg ctg agc cct gag ctg cgt			
1075			
Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu Ser Pro Glu Leu Arg			
310	315	320	325
gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct			
1123			
Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro			
	330	335	340
gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac			
1171			
Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp			
	345	350	355
cgt aat ggc ctg cga cct ggg cga atc acc att act gat tgc ggt ttg			
1219			
Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu			
	360	365	370
gtt gtg atg gct tct gaa tgc gga gtg ttg gac ttg agg gag gag agc			
1267			
Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser			
	375	380	385
gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac			
1315			
Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp			
390	395	400	405
act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta			
1363			
Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu			
	410	415	420

agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat  
1411

Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His  
425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt  
1459

Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg  
440 445 450

gct gtg ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat  
1507

Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp  
455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc  
1555

Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser  
470 475 480 485

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg  
1603

Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met  
490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg  
1651

Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro  
505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg  
1699

Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu  
520 525 530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt  
1747

Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg  
535 540 545

atc cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg  
1795

Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu  
550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta  
1843

Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val  
570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc gcc atg aag gct  
1891

Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala  
585 590 595

gcg att gct cgt gtg cgc cgc gag gtt tct gaa gca atc cgc aat ggc  
1939

Ala Ile Ala Arg Val Arg Arg Glu Val Ser Glu Ala Ile Arg Asn Gly  
600 605 610

aag acg ttg atc gtg ctg tgc gat cgt gaa tct gat gag cgc atg gca  
1987

Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser Asp Glu Arg Met Ala  
615 620 625

cct atc cct gcg ctg ctg ctg act tcc gct gtg cat cag tac ttg gtg  
2035

Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val His Gln Tyr Leu Val  
630 635 640 645

cag caa cgt acc cgt acc cag tgc tcc ctg gtg gtg gaa tcc ggc gat  
2083

Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val Val Glu Ser Gly Asp  
650 655 660

gcc cgc gag gtt cat cac ctg gcg atg ctc att ggt ttt ggt gcc gat  
2131

Ala Arg Glu Val His His Leu Ala Met Leu Ile Gly Phe Gly Ala Asp  
665 670 675

gcg atc aac ccg tac atg gca ttt gaa acc atc gat gag ctg cgc atg  
2179

Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile Asp Glu Leu Arg Met  
680 685 690

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2227

Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu Ala Ser Arg Asn Tyr  
695 700 705

atc aag gca gcc acc act ggt gtg ctg aag gtg atg tcc aag atg ggc  
2275

Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val Met Ser Lys Met Gly  
710 715 720 725

att gca acg gtg tct tgc tac cgt ggc gcg cag ctt gcc gat gtc act  
2323

Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln Leu Ala Asp Val Thr  
730 735 740

ggt ctg cac cag gat ctc ctg gac aac tac ttc ggt ggt att gct tca  
2371

Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe Gly Gly Ile Ala Ser  
745 750 755

cca att tct ggc atc ggt ctg gat gaa gtt gca gct gac gta gaa gct  
2419

Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala Ala Asp Val Glu Ala  
760 765 770

cgt cac cgc agc gca ttt ttg cca cgc cct gaa gag cac gct cac cgt  
2467

Arg His Arg Ser Ala Phe Leu Pro Arg Pro Glu Glu His Ala His Arg  
775 780 785

gaa ttg gat ttg ggt ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac  
2515

Glu Leu Asp Leu Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr  
790 795 800 805

cac ctg ttc aac cca gaa acc atc ttc aag ctg cag cat gca acg cgt  
2563

His Leu Phe Asn Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg  
810 815 820

tct ggc agc tac gag att ttc aag gat tac acc cgc aag gtt gat gat  
2611

Ser Gly Ser Tyr Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp  
825 830 835

caa tcc act cgc ttg ggt act att cgt gga ctg ttt gag ttc agc acg  
2659

Gln Ser Thr Arg Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr  
840 845 850

gac cgc aag cca att tcg gtg tct gag gtg gag ccg gtc agt gag atc  
2707

Asp Arg Lys Pro Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile  
855 860 865

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Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala  
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gaa gcc cat gag gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg  
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Glu Ala His Glu Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met  
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tcc aac tcc ggc gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa  
2851

Ser Asn Ser Gly Glu Gly Gly Glu Asp Ala Arg Arg Phe Asp Val Glu  
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2899

Pro Asn Gly Asp Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly  
920 925 930

cgt ttc ggc gtg acc agc cac tac ttg aac aac tgc acc gat att cag  
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Arg Phe Gly Val Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln  
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Ile Lys Met Ala Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro  
950 955 960 965

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Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro  
970 975 980

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 Ala Ala Gly Val Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly  
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 Arg Val Cys His Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn  
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Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu  
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3763  
Ser Pro Ile Phe His Arg Pro Glu Thr Pro His Phe Pro Thr Gln Asp  
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Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu Glu Lys Ala Leu Asp  
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1270 1275 1280 1285  
  
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4003  
Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu Asn Leu Gln Gly Cys  
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4099  
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Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro Lys Gln Leu Lys Asn  
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Gly Glu Leu Phe Ile Arg Gly Gln Val Gly Glu Arg Phe Cys Val Arg  
1370 1375 1380

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4291

Asn Ser Gly Ala Thr Ala Val Val Glu Gly Ile Gly Asn His Gly Cys  
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4339

Glu Tyr Met Thr Gly Gly Arg Val Leu Val Leu Gly Pro Val Gly Glu  
1400 1405 1410

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4387

Asn Phe Gly Ala Gly Met Ser Gly Gly Ile Ala Tyr Leu Ala Asn Ser  
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Pro Asp Leu Asn Gln Lys Ile Asn Gly Glu Leu Val Asp Val Val Pro  
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1450 1455 1460

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Arg Glu Leu Thr Gly Ser Glu Thr Lys Leu Arg Ala Gln Asp Leu Val  
1465 1470 1475

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4627

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<400> 72

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20 25 30

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35 40 45

Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln  
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 Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu  
 65 70 75 80  
 Ala Gly Glu Tyr Ala Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met  
 85 90 95  
 Ala Met Met Asp Ala Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu  
 100 105 110  
 Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp  
 115 120 125  
 Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe  
 130 135 140  
 Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe  
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 Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys  
 180 185 190  
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 Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val  
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 260 265 270  
 Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe  
 275 280 285  
 Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His  
 290 295 300  
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 Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu  
 325 330 335  
 Pro Trp Asp Gly Pro Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val  
 340 345 350  
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 355 360 365  
 Thr Asp Ser Gly Leu Val Val Met Ala Ser Glu Ser Gly Val Leu Asp

370	375	380
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Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu 405 410 415		
Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg 420 425 430		
Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr 435 440 445		
Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr 450 455 460		
Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala 465 470 475 480		
Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser 485 490 495		
Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln 500 505 510		
Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser 515 520 525		
Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro 530 535 540		
Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His 545 550 555 560		
Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser 565 570 575		
Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly 580 585 590		
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Ala Ile Arg Asn Gly Lys Thr Leu Ile Val Leu Ser Asp Arg Glu Ser 610 615 620		
Asp Glu Arg Met Ala Pro Ile Pro Ala Leu Leu Leu Thr Ser Ala Val 625 630 635 640		
His Gln Tyr Leu Val Gln Gln Arg Thr Arg Thr Gln Cys Ser Leu Val 645 650 655		
Val Glu Ser Gly Asp Ala Arg Glu Val His His Leu Ala Met Leu Ile 660 665 670		
Gly Phe Gly Ala Asp Ala Ile Asn Pro Tyr Met Ala Phe Glu Thr Ile 675 680 685		
Asp Glu Leu Arg Met Lys Gly Gln Leu Gly Asp Leu Ser Leu Asp Glu 690 695 700		

Ala Ser Arg Asn Tyr Ile Lys Ala Ala Thr Thr Gly Val Leu Lys Val  
 705 710 715 720  
 Met Ser Lys Met Gly Ile Ala Thr Val Ser Ser Tyr Arg Gly Ala Gln  
 725 730 735  
 Leu Ala Asp Val Thr Gly Leu His Gln Asp Leu Leu Asp Asn Tyr Phe  
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 Gly Gly Ile Ala Ser Pro Ile Ser Gly Ile Gly Leu Asp Glu Val Ala  
 755 760 765  
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 770 775 780  
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 Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr Gly Ala Met Ser Tyr  
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 Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu Ala Ile Ala Met Asn  
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 Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro Trp Val Ala Glu Val  
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 Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp Glu Ala Val Gly Gln  
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 Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro Ala Asp Ser Arg Ala  
 1185 1190 1195 1200  
 Ala His Leu Asp Leu Ser Pro Ile Phe His Arg Pro Glu Thr Pro His  
 1205 1210 1215  
 Phe Pro Thr Gln Asp Val Arg Cys Thr Lys Thr Gln Glu His Ser Leu  
 1220 1225 1230  
 Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser Asp Thr Ile  
 1235 1240 1245  
~~Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile Asp Ser Ser~~  
~~1250 1255 1260~~  
 Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly Ser Ala Val  
 1265 1270 1275 1280  
 Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr Ile Thr Leu  
 1285 1290 1295  
 Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe Ile Pro Arg  
 1300 1305 1310  
 Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe Val Gly Lys  
 1315 1320 1325  
 Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala Gln Ala Pro  
 1330 1335 1340  
 Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn Val Leu Gly

113

aac act ggc gat ggt gcg ggc atc ctc atg cag att ccg gac ggc ttt 307  
 Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln Ile Pro Asp Gly Phe  
 55 60 65

tat cgt gaa gta tct ggc att gag ctt cct gag gca ggg gag tat gcc 355  
 Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu Ala Gly Glu Tyr Ala  
 70 75 80 85

act ggt att gcg ttc ttg cct cgc ggt cgc atg gcg atg atg gat gct 403  
 Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met Ala Met Met Asp Ala  
 90 95 100

cag aag gaa att gag cgc atc gca aag caa gaa ggt gcc gat gtg ctt 451  
 Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu Gly Ala Asp Val Leu  
 105 110 115

ggt tgg cgc atg gtt cct ttt gat tct cgt gat ttg ggt tcc atg gct 499  
 Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp Leu Gly Ser Met Ala  
 120 125 130

gag gag gcg atg cct agt ttc gcg cag att ttc ctt act gtg cct gga 547  
 Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe Leu Thr Val Pro Gly  
 135 140 145

aaa tct ggt gaa gat ctt gac cgt gtg atg ttc ttt atc cgt aag cgt 595  
 Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe Phe Ile Arg Lys Arg  
 150 155 160 165

tgt gag cgt gag ctg ggc acc acc aat ggt cgc gat acg gtg tat ttc 643  
 Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg Asp Thr Val Tyr Phe  
 170 175 180

ccg tcg cta tct tca cgc acc atc att tac aaa ggc atg ttg acc act 691  
 Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys Gly Met Leu Thr Thr  
 185 190 195

ctg cag ctt gag ggc ttc ttt gag gat ctg ggt gat gct cgc ctg gag 739  
 Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly Asp Ala Arg Leu Glu  
 200 205 210

tcg gcc att gct att gtg cac tcg cgt ttc tcc acg aac act ttc cca 787  
 Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser Thr Asn Thr Phe Pro  
 215 220 225

agc tgg ccg ctg gcg cac ccg tac cgt ttc gtt gcc cac aac ggt gag 835  
 Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val Ala His Asn Gly Glu  
 230 235 240 245

atc aac act gtg cgt ggc aat gaa aac tgg atg cgc gcc cgc gag gcg 883  
 Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met Arg Ala Arg Glu Ala  
 250 255 260

ctt atc aaa aac gac aag ctg ggc aat ttg agc agc gtg ctg cct atc 931  
 Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser Ser Val Leu Pro Ile  
 265 270 275

tgc acc ccg gag ggc tcg gat acc gcg cgt ttc gac gag gct ttg gag 979  
 Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe Asp Glu Ala Leu Glu  
 280 285 290

ctt ttg cac ctg ggc gga tac tca ctt ccg cat gct gtt gcg atg atg  
 1027  
 Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His Ala Val Ala Met Met  
 295 300 305

atc cct cag gcg tgg gaa cac aac aag acg ctg agc cct gag ctg cgt  
 1075  
 Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu Ser Pro Glu Leu Arg  
 310 315 320 325

gat ttc tac gaa tac cac tct tgt ctg atg gag cca tgg gat ggt cct  
 1123  
 Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu Pro Trp Asp Gly Pro  
 330 335 340

gca gcg ctg gca ttt act gac ggt cgt ttt gtg ggt gcc gtg ctg gac  
 1171  
 Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val Gly Ala Val Leu Asp  
 345 350 355

cgt aat ggc ctg cga cct ggg cga atc acc att act gat tcg ggt ttg  
 1219  
 Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile Thr Asp Ser Gly Leu  
 360 365 370

gtt gtg atg gct tct gaa tcg gga gtg ttg gac ttg agg gag gag agc  
 1267  
 Val Val Met Ala Ser Glu Ser Gly Val Leu Asp Leu Arg Glu Glu Ser  
 375 380 385

gtc gta aag cgt act cgc gta cag cct gga cgc atg ttc ctt gtt gac  
 1315  
 Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg Met Phe Leu Val Asp  
 390 395 400 405

act gcc gag ggc cgc atc gtt gaa gac gag gaa atc aag cag aaa tta  
 1363  
 Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu Ile Lys Gln Lys Leu  
 410 415 420

agc gaa gcg cag cca tat ggt gag tgg att cgc gat aat ttt gtg cat  
 1411  
 Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg Asp Asn Phe Val His  
 425 430 435

ctg gat cgt ctg cct cag aca cgc tac aac tac atg gcg cac tct cgt  
 1459  
 Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr Met Ala His Ser Arg  
 440 445 450

gct gty ttg cgt cag cgt gtt ttc gga atc act gaa gaa gat gtg gat  
 1507  
 Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr Glu Glu Asp Val Asp  
 455 460 465

ttg ttg ctg ctg ccg atg gcc cgc cag ggt gct gag gcg att ggt tcc  
 1555  
 Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala Glu Ala Ile Gly Ser  
 470 475 480 485

atg ggt tcg gat acg cca att gcg gcg cta tcc cag cga cca cgc atg  
1603

Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser Gln Arg Pro Arg Met  
490 495 500

ctt tat gat ttc ttc gcg cag cgc ttt gct cag gtg aca aac cca ccg  
1651

Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln Val Thr Asn Pro Pro  
505 510 515

ttg gac tct atc cgc gaa aag cct gtg acc agc atg ttc act ttg ttg  
1699

Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser Met Phe Thr Leu Leu  
520 525 530

ggt gcg cag tct gac gtg ctc aat ccg ggt cct gat gcg gcg cga cgt  
1747

Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro Asp Ala Ala Arg Arg  
535 540 545

att cgt ttg gaa tcg ccg atc att gat aac cat gag ctg gcc acc ttg  
1795

Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His Glu Leu Ala Thr Leu  
550 555 560 565

atc aat gcc aac gcg cat ggt gag tgg gat tcc ttt ggt gct gct gta  
1843

Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser Phe Gly Ala Ala Val  
570 575 580

att tct ggt ttg tac cca gtg gct cac cat ggt gcc ggc atg aag gct  
1891

Ile Ser Gly Leu Tyr Pro Val Ala His His Gly Ala Gly Met Lys Ala  
585 590 595

gcg att gct cgt gtg  
1906

Ala Ile Ala Arg Val  
600

<210> 74

<211> 602

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

Met Lys Pro Gln Gly Leu Tyr Asn Pro Ala His Glu His Asp Ala Cys  
1 5 10 15

Gly Val Ala Phe Ile Ala Asp Ile His Gly Arg Pro Ser Arg Ser Ile  
20 25 30

Val Asp Arg Ala Leu Glu Ala Leu Arg Asn Ile Asp His Arg Gly Ala  
35 40 45

Ala Gly Ala Glu Lys Asn Thr Gly Asp Gly Ala Gly Ile Leu Met Gln  
50 55 60

Ile Pro Asp Gly Phe Tyr Arg Glu Val Ser Gly Ile Glu Leu Pro Glu  
65 70 75 80

Ala Gly Glu Tyr Ala Thr Gly Ile Ala Phe Leu Pro Arg Gly Arg Met  
                             85                            90                            95  
 Ala Met Met Asp Ala Gln Lys Glu Ile Glu Arg Ile Ala Lys Gln Glu  
                             100                            105                            110  
 Gly Ala Asp Val Leu Gly Trp Arg Met Val Pro Phe Asp Ser Arg Asp  
                             115                            120                            125  
 Leu Gly Ser Met Ala Glu Glu Ala Met Pro Ser Phe Ala Gln Ile Phe  
                             130                            135                            140  
 Leu Thr Val Pro Gly Lys Ser Gly Glu Asp Leu Asp Arg Val Met Phe  
                             145                            150                            155                            160  
 Phe Ile Arg Lys Arg Cys Glu Arg Glu Leu Gly Thr Thr Asn Gly Arg  
                             165                            170                            175  
 Asp Thr Val Tyr Phe Pro Ser Leu Ser Ser Arg Thr Ile Ile Tyr Lys  
                             180                            185                            190  
 Gly Met Leu Thr Thr Leu Gln Leu Glu Gly Phe Phe Glu Asp Leu Gly  
                             195                            200                            205  
 Asp Ala Arg Leu Glu Ser Ala Ile Ala Ile Val His Ser Arg Phe Ser  
                             210                            215                            220  
 Thr Asn Thr Phe Pro Ser Trp Pro Leu Ala His Pro Tyr Arg Phe Val  
                             225                            230                            235                            240  
 Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn Glu Asn Trp Met  
                             245                            250                            255  
 Arg Ala Arg Glu Ala Leu Ile Lys Asn Asp Lys Leu Gly Asn Leu Ser  
                             260                            265                            270  
 Ser Val Leu Pro Ile Cys Thr Pro Glu Gly Ser Asp Thr Ala Arg Phe  
                             275                            280                            285  
 Asp Glu Ala Leu Glu Leu Leu His Leu Gly Gly Tyr Ser Leu Pro His  
                             290                            295                            300  
 Ala Val Ala Met Met Ile Pro Gln Ala Trp Glu His Asn Lys Thr Leu  
                             305                            310                            315                            320  
 Ser Pro Glu Leu Arg Asp Phe Tyr Glu Tyr His Ser Cys Leu Met Glu  
                             325                            330                            335  
 Pro Trp Asp Gly Pro Ala Ala Leu Ala Phe Thr Asp Gly Arg Phe Val  
                             340                            345                            350  
 Gly Ala Val Leu Asp Arg Asn Gly Leu Arg Pro Gly Arg Ile Thr Ile  
                             355                            360                            365  
 Thr Asp Ser Gly Leu Val Val Met Ala Ser Glu Ser Gly Val Leu Asp  
                             370                            375                            380  
 Leu Arg Glu Glu Ser Val Val Lys Arg Thr Arg Val Gln Pro Gly Arg  
                             385                            390                            395                            400

Met Phe Leu Val Asp Thr Ala Glu Gly Arg Ile Val Glu Asp Glu Glu  
405 410 415

Ile Lys Gln Lys Leu Ser Glu Ala Gln Pro Tyr Gly Glu Trp Ile Arg  
420 425 430

Asp Asn Phe Val His Leu Asp Arg Leu Pro Gln Thr Arg Tyr Asn Tyr  
435 440 445

Met Ala His Ser Arg Ala Val Leu Arg Gln Arg Val Phe Gly Ile Thr  
450 455 460

Glu Glu Asp Val Asp Leu Leu Leu Leu Pro Met Ala Arg Gln Gly Ala  
465 470 475 480

Glu Ala Ile Gly Ser Met Gly Ser Asp Thr Pro Ile Ala Ala Leu Ser  
485 490 495

Gln Arg Pro Arg Met Leu Tyr Asp Phe Phe Ala Gln Arg Phe Ala Gln  
500 505 510

Val Thr Asn Pro Pro Leu Asp Ser Ile Arg Glu Lys Pro Val Thr Ser  
515 520 525

Met Phe Thr Leu Leu Gly Ala Gln Ser Asp Val Leu Asn Pro Gly Pro  
530 535 540

Asp Ala Ala Arg Arg Ile Arg Leu Glu Ser Pro Ile Ile Asp Asn His  
545 550 555 560

Glu Leu Ala Thr Leu Ile Asn Ala Asn Ala His Gly Glu Trp Asp Ser  
565 570 575

Phe Gly Ala Ala Val Ile Ser Gly Leu Tyr Pro Val Ala His His Gly  
580 585 590

Ala Gly Met Lys Ala Ala Ile Ala Arg Val  
595 600

<210> 75

<211> 1362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (70)..(1362)

<223> FRXA00364

<400> 75

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ggcatttttttg cca cgc cct gaa gag cac gct cac cgt gaa ttg gat ttg 111

Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu

1

5

10

ggg ggt gaa tac aag tgg cgc cgc gaa ggt gaa tac cac ctg ttc aac 159

Gly Gly Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn

15

20

25

30

cca gaa acc atc ttc aag ctg cag cat gca acg cgt tct ggc agc tac	207
Pro Glu Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr	
35 40 45	
gag att ttc aag gat tac acc cgc aag gtt gat gat caa tcc act cgc	255
Glu Ile Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg	
50 55 60	
ttg ggt act att cgt gga ctg ttt gag ttc agc acg gac cgc aag cca	303
Leu Gly Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro	
65 70 75	
att tcg gtg tct gag gtg gag ccg gtc agt gag atc gtg aag cgt ttc	351
Ile Ser Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe	
80 85 90	
tcc act ggt gcg atg tct tat ggc tcg att tct gct gaa gcc cat gag	399
Ser Thr Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu	
95 100 105 110	
gtc ttg gcc atc gcc atg aac cga ctg ggc ggt atg tcc aac tcc ggc	447
Val Leu Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly	
115 120 125	
gaa ggt ggc gag gac gcc cgc cga ttt gat gtg gaa ccc aac ggt gac	495
Glu Gly Gly Glu Asp Ala Arg Phe Asp Val Glu Pro Asn Gly Asp	
130 135 140	
tgg aag cgc tct gcc att aag cag gtg gcc tcg gga cgt ttc ggc gtg	543
Trp Lys Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val	
145 150 155	
acc agc cac tac ttg aac aac tgc acc gat att cag atc aag atg gca	591
Thr Ser His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala	
160 165 170	
cag ggc gca aag ccc ggt gaa ggt ggc cag ctg cca cca aac aag gtg	639
Gln Gly Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val	
175 180 185 190	
tac cca tgg gtt gca gaa gtc cgc atc acc acc cca ggc gtt ggt ctg	687
Tyr Pro Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu	
195 200 205	
att tcc cct cca cca cac cac gat att tac tcc att gag gat ctg gct	735
Ile Ser Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala	
210 215 220	
cag ctg atc cac gac ctg aag aac gct aac cca cgc gca cga atc cac	783
Gln Leu Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His	
225 230 235	
gtg aag cta gtg gca gaa caa ggc gtg ggc acc gtt gcc gca ggt gtg	831
Val Lys Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val	
240 245 250	
tcc aaa gca cac gct gat gtg gtg ctt att tcc ggc cac gat ggc gga	879
Ser Lys Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly	
255 260 265 270	
act ggc gca tct cct ttg acc tcc ctg aag cat gcc ggt ggt cca tgg	927

Thr Gly Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp  
 275 280 285

gag ttg ggc ttg gct gaa acc cag caa acg ttg ctg ctc aac ggc ctg 975  
 Glu Leu Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu  
 290 295 300

cgc gat cgt att cgc gtg cag tgc gat ggt cag ctg aaa act ggc cga  
 1023  
 Arg Asp Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg  
 305 310 315

gac gtg gtt atc gca gct ctt ctc ggt gcc gaa gaa ttc ggt ttt gcc  
 1071  
 Asp Val Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala  
 320 325 330

acc gca ccg ctg gtg gtt gaa ggc tgc atc atg atg cgc gtc tgc cac  
 1119  
 Thr Ala Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His  
 335 340 345 350

ctg gac acc tgc ccg gtg ggt atc gct acc cag aac ccg gat ttg cgt  
 1167  
 Leu Asp Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg  
 355 360 365

tcc aag ttc acc ggc aag gct gaa cac gtg gtc aac ttc ttc acc ttc  
 1215  
 Ser Lys Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe  
 370 375 380

atc gcc cag gaa gtc cgt gag tac ttg gca cag ctt ggt ttc cgc tct  
 1263  
 Ile Ala Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser  
 385 390 395

att gat gaa gcc gtc gga caa gcc cag gtg ctg cgc aag cgt tcc gga  
 1311  
 Ile Asp Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly  
 400 405 410

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atc cca gct gat tcc cgc gca gca cac ctg gat ttg agc cca att ttc  
 1359  
 Ile Pro Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe  
 415 420 425 430

atc  
 1362  
 Ile

<210> 76  
 <211> 431  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 76  
 Leu Pro Arg Pro Glu Glu His Ala His Arg Glu Leu Asp Leu Gly Gly  
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Glu Tyr Lys Trp Arg Arg Glu Gly Glu Tyr His Leu Phe Asn Pro Glu  
                   20                                  25                                  30  
 Thr Ile Phe Lys Leu Gln His Ala Thr Arg Ser Gly Ser Tyr Glu Ile  
                   35                                  40                                  45  
 Phe Lys Asp Tyr Thr Arg Lys Val Asp Asp Gln Ser Thr Arg Leu Gly  
                   50                                  55                                  60  
 Thr Ile Arg Gly Leu Phe Glu Phe Ser Thr Asp Arg Lys Pro Ile Ser  
                   65                                  70                                  75                                  80  
 Val Ser Glu Val Glu Pro Val Ser Glu Ile Val Lys Arg Phe Ser Thr  
                                   85                                  90                                  95  
 Gly Ala Met Ser Tyr Gly Ser Ile Ser Ala Glu Ala His Glu Val Leu  
                                   100                                  105                                  110  
 Ala Ile Ala Met Asn Arg Leu Gly Gly Met Ser Asn Ser Gly Glu Gly  
                                   115                                  120                                  125  
 Gly Glu Asp Ala Arg Arg Phe Asp Val Glu Pro Asn Gly Asp Trp Lys  
                   130                                  135                                  140  
 Arg Ser Ala Ile Lys Gln Val Ala Ser Gly Arg Phe Gly Val Thr Ser  
                   145                                  150                                  155                                  160  
 His Tyr Leu Asn Asn Cys Thr Asp Ile Gln Ile Lys Met Ala Gln Gly  
                                   165                                  170                                  175  
 Ala Lys Pro Gly Glu Gly Gly Gln Leu Pro Pro Asn Lys Val Tyr Pro  
                                   180                                  185                                  190  
 Trp Val Ala Glu Val Arg Ile Thr Thr Pro Gly Val Gly Leu Ile Ser  
                   195                                  200                                  205  
 Pro Pro Pro His His Asp Ile Tyr Ser Ile Glu Asp Leu Ala Gln Leu  
                   210                                  215                                  220  
 Ile His Asp Leu Lys Asn Ala Asn Pro Arg Ala Arg Ile His Val Lys  
                   225                                  230                                  235                                  240  
 Leu Val Ala Glu Gln Gly Val Gly Thr Val Ala Ala Gly Val Ser Lys  
                                   245                                  250                                  255  
 Ala His Ala Asp Val Val Leu Ile Ser Gly His Asp Gly Gly Thr Gly  
                                   260                                  265                                  270  
 Ala Ser Pro Leu Thr Ser Leu Lys His Ala Gly Gly Pro Trp Glu Leu  
                   275                                  280                                  285  
 Gly Leu Ala Glu Thr Gln Gln Thr Leu Leu Leu Asn Gly Leu Arg Asp  
                   290                                  295                                  300  
 Arg Ile Arg Val Gln Cys Asp Gly Gln Leu Lys Thr Gly Arg Asp Val  
                   305                                  310                                  315                                  320  
 Val Ile Ala Ala Leu Leu Gly Ala Glu Glu Phe Gly Phe Ala Thr Ala  
                                   325                                  330                                  335

Pro Leu Val Val Glu Gly Cys Ile Met Met Arg Val Cys His Leu Asp  
 340 345 350

Thr Cys Pro Val Gly Ile Ala Thr Gln Asn Pro Asp Leu Arg Ser Lys  
 355 360 365

Phe Thr Gly Lys Ala Glu His Val Val Asn Phe Phe Thr Phe Ile Ala  
 370 375 380

Gln Glu Val Arg Glu Tyr Leu Ala Gln Leu Gly Phe Arg Ser Ile Asp  
 385 390 395 400

Glu Ala Val Gly Gln Ala Gln Val Leu Arg Lys Arg Ser Gly Ile Pro  
 405 410 415

Ala Asp Ser Arg Ala Ala His Leu Asp Leu Ser Pro Ile Phe Ile  
 420 425 430

&lt;210&gt; 77

&lt;211&gt; 866

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(843)

&lt;223&gt; FRXA00367

&lt;400&gt; 77

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 His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser  
 1 5 10 15

gac acg atc acc cgt gcc gca gcg ggt gtg gaa acc agc att gtt att 96  
 Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile  
 20 25 30

gat agc tcc atc agc aac gtc aac cgt tca gtt ggc acg atg ctg ggt 144  
 Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly  
 35 40 45

tct gca gtc agc cgc gtg gct ggt gcc caa ggt ttg cca gac ggc acc 192  
 Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr  
 50 55 60

atc acc ttg aat ctt caa ggc tgc gcc ggt aac tcc ttt ggc gcg ttc 240  
 Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe  
 65 70 75 80

atc cca cga ggc atc acc atc aac ctc acc ggc gat gcc aat gac ttt 288  
 Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe  
 85 90 95

gtg ggc aag gga tta tct ggc gga aag att gtg atc aag cct tcc gct 336  
 Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala  
 100 105 110

cag gct ccg aag cag ctg aag aac aat cca aat atc att gcc gga aac 384  
 Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn  
 115 120 125

gtg ctt gga tac ggc gca acc agt ggt gaa ttg ttc att cgt ggc cag 432  
Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln  
130 135 140

gtc ggc gaa cgt ttc tgc gtc cgt aac tct ggc gcc acc gca gtg gtt 480  
Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val  
145 150 155 160

gaa ggt atc gga aac cac ggt tgt gag tac atg act ggc ggc cga gtc 528  
Glu Gly Ile Gly Asn His Gly Asn Glu Tyr Met Thr Gly Gly Arg Val  
165 170 175

ctg gtt ttg ggc ccg gtt ggt gag aac ttt ggt gcc ggc atg tct ggt 576  
Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly  
180 185 190

ggc att gca tac ctg gct aat tcc ccg gac cta aac cag aag atc aat 624  
Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn  
195 200 205

ggc gaa ttg gtg gat gtt gtt cca ctg agc gct gac gat ctg acg tgg 672  
Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp  
210 215 220

gct gat gag ctc att gct cgc cac cgc gaa ctc acc gga tcc gag acc 720  
Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr  
225 230 235 240

aag ctg cgt gca caa gat ttg gtg aaa atc atg ccg cgc gat ttc caa 768  
Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln  
245 250 255

aaa gta ctc aac atc atc gaa acg gcc cac gct gag ggc caa gac cca 816  
Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro  
260 265 270

gca atc aag atc atg gag gca gtg agc taatggccga cccacaagga 863  
Ala Ile Lys Ile Met Glu Ala Val Ser  
275 280

ttc 866

&lt;210&gt; 78

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 78

His Ser Leu Glu Lys Ala Leu Asp Asn Ala Phe Ile Asp Lys Ala Ser  
1 5 10 15

Asp Thr Ile Thr Arg Ala Ala Ala Gly Val Glu Thr Ser Ile Val Ile  
20 25 30

Asp Ser Ser Ile Ser Asn Val Asn Arg Ser Val Gly Thr Met Leu Gly  
35 40 45

Ser Ala Val Ser Arg Val Ala Gly Ala Gln Gly Leu Pro Asp Gly Thr  
50 55 60

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Ile Thr Leu Asn Leu Gln Gly Cys Ala Gly Asn Ser Phe Gly Ala Phe
 65              70              75              80

Ile Pro Arg Gly Ile Thr Ile Asn Leu Thr Gly Asp Ala Asn Asp Phe
              85              90              95

Val Gly Lys Gly Leu Ser Gly Gly Lys Ile Val Ile Lys Pro Ser Ala
              100             105             110

Gln Ala Pro Lys Gln Leu Lys Asn Asn Pro Asn Ile Ile Ala Gly Asn
              115             120             125

Val Leu Gly Tyr Gly Ala Thr Ser Gly Glu Leu Phe Ile Arg Gly Gln
              130             135             140

Val Gly Glu Arg Phe Cys Val Arg Asn Ser Gly Ala Thr Ala Val Val
              145             150             155             160

Glu Gly Ile Gly Asn His Gly Cys Glu Tyr Met Thr Gly Gly Arg Val
              165             170             175

Leu Val Leu Gly Pro Val Gly Glu Asn Phe Gly Ala Gly Met Ser Gly
              180             185             190

Gly Ile Ala Tyr Leu Ala Asn Ser Pro Asp Leu Asn Gln Lys Ile Asn
              195             200             205

Gly Glu Leu Val Asp Val Val Pro Leu Ser Ala Asp Asp Leu Thr Trp
              210             215             220

Ala Asp Glu Leu Ile Ala Arg His Arg Glu Leu Thr Gly Ser Glu Thr
              225             230             235             240

Lys Leu Arg Ala Gln Asp Leu Val Lys Ile Met Pro Arg Asp Phe Gln
              245             250             255

Lys Val Leu Asn Ile Ile Glu Thr Ala His Ala Glu Gly Gln Asp Pro
              260             265             270

Ala Ile Lys Ile Met Glu Ala Val Ser
              275             280

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<210> 79
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1471)
<223> RXN00076

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<400> 79
tctaggagtg ttaaacagcc tggacttgaa acacctttaa ctacttgatt ttcacaccct 60

tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115
              Met Thr Thr Pro Leu
              1              5

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cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac	163
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp	
10 15 20	
ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag	211
Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu	
25 30 35	
caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac	259
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp	
40 45 50	
cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac	307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp	
55 60 65	
aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc	355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile	
70 75 80 85	
acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc	403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr	
90 95 100	
ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa	451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu	
105 110 115	
ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca	499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro	
120 125 130	
cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc	547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile	
135 140 145	
ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca	595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr	
150 155 160 165	
ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc	643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser	
170 175 180	
ctc aaa gaa aac aag gcc act gaa gtg cac gtt ttc gga cgt cgt ggc	691
Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly	
185 190 195	
cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac	739
Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His	
200 205 210	
tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac	787
Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu Asp Ile Asp Tyr Asp	
215 220 225	
ggc gcc tct gaa gaa gcc cgc cgc gca tcc aag tcc cag gac ctg gtc	835
Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val	
230 235 240 245	
tgc cag atc ctg gaa cag tac gca atc cgc gag cca aag gac gct ccg	883

Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro  
 250 255 260

cac acc ctg cag atc cac ctc ttt gaa aac cca gtt gag gtt ctt caa 931  
 His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln  
 265 270 275

aag gac ggc aag gtt gtt ggc ctg cgc acc gaa cgc acc tca ctt gat 979  
 Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp  
 280 285 290

ggc aac ggc ggc gta aac gga acc ggc gaa ttc aag gac tgg cca ttc  
 1027  
 Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe Lys Asp Trp Pro Val  
 295 300 305

cag gct gtc tac cgc gca gtc ggc tac aag tcc gac ccc atc gac ggc  
 1075  
 Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser Asp Pro Ile Asp Gly  
 310 315 320 325

gtc cca ttc gat gag aac aag cac gtc atc cct aat gac ggc gga cat  
 1123  
 Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His  
 330 335 340

gtc ctc acc gct cca ggc gca gaa cca gta cca ggc ctc tat gca acc  
 1171  
 Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro Gly Leu Tyr Ala Thr  
 345 350 355

ggc tgg atc aag cgt gga cca atc ggt cta atc ggc aac acc aag tcc  
 1219  
 Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser  
 360 365 370

gac gcc aag gaa acc acc gac atc ctc atc aag gat gcc gtc gcc ggt  
 1267  
 Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys Asp Ala Val Ala Gly  
 375 380 385

gta ctt gaa gct cca aag cac cag ggc gaa gaa gcc atc atc gag ctt  
 1315  
 Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu  
 390 395 400 405

ctc gat tcc cgc aac atc cca ttc acc acc tgg gaa ggc tgg tac aaa  
 1363  
 Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp Glu Gly Trp Tyr Lys  
 410 415 420

ctc gac gca gca gag cgc gca ctc ggt gaa gcc gaa ggc cgc gag cgc  
 1411  
 Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala Glu Gly Arg Glu Arg  
 425 430 435

aag aag att gtt gat tgg gaa gaa atg gtc cgc cag gcc cgc gaa gct  
 1459  
 Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala  
 440 445 450

cca gca att gtc taaattgttt taacgcgtga agc

1494

Pro Ala Ile Val

455

<210> 80

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly  
1 5 10 15

Ile Tyr Ala Ser Asp Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe  
20 25 30

Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr  
35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu  
50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu  
65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala  
85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro  
100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe  
115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln  
130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg  
145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp  
165 170 175

Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val  
180 185 190

Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu  
195 200 205

Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu  
210 215 220

Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys  
225 230 235 240

Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu  
245 250 255

Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro

260 265 270  
 Val Glu Val Leu Gln Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu  
 275 280 285  
 Arg Thr Ser Leu Asp Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe  
 290 295 300  
 Lys Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser  
 305 310 315 320  
 Asp Pro Ile Asp Gly Val Pro Phe Asp Glu Asn Lys His Val Ile Pro  
 325 330 335  
 Asn Asp Gly Gly His Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro  
 340 345 350  
 Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile  
 355 360 365  
 Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys  
 370 375 380  
 Asp Ala Val Ala Gly Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu  
 385 390 395 400  
 Ala Ile Ile Glu Leu Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp  
 405 410 415  
 Glu Gly Trp Tyr Lys Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala  
 420 425 430  
 Glu Gly Arg Glu Arg Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg  
 435 440 445  
 Gln Ala Arg Glu Ala Pro Ala Ile Val  
 450 455

&lt;210&gt; 81

&lt;211&gt; 786

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(763)

&lt;223&gt; FRXA00075

&lt;400&gt; 81

tctaggagtg ttaaacagcc tggacttgaa acacctttaa ctacttgatt ttcacaccct 60

tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115  
 Met Thr Thr Pro Leu  
 1 5

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac 163  
 Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp  
 10 15 20

ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211

Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu  
                   25                                  30                                  35

caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac 259  
 Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp  
                   40                                  45                                  50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307  
 His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp  
                   55                                  60                                  65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc 355  
 Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile  
                   70                                  75                                  80                                  85

acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc 403  
 Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr  
                                   90                                  95                                  100

ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa 451  
 Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu  
                                   105                                  110                                  115

ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca 499  
 Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro  
                   120                                  125                                  130

cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc 547  
 Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile  
                   135                                  140                                  145

ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca 595  
 Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr  
                                   155                                  160                                  165

ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc 643  
 Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser  
                                   170                                  175                                  180

ctc aaa gaa aac aag gyc wct gaa gtg cac gtt ttc gga cgt cgg tgg 691  
 Leu Lys Glu Asn Lys Xaa Xaa Glu Val His Val Phe Gly Arg Arg Trp  
                                   185                                  190                                  195

ccc agc aca ggt caa gtt cac ccc aca gga act maa aga act cgr cca 739  
 Pro Ser Thr Gly Gln Val His Pro Thr Gly Thr Xaa Arg Thr Xaa Pro  
                   200                                  205                                  210

ctc ccc cac cat caa cgt ggt tgt tgatccagaa gacatcgact acg 786  
 Leu Pro His His Gln Arg Gly Cys  
                   215                                  220

<210> 82  
 <211> 221  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 82  
 Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly  
                   1                                  5                                  10                                  15

<210> 83

<211> 672

~~212~~ DIVA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$ 

<221> CDS

$\langle 222 \rangle$  (101) . . (649)

<223> RXN00198

<400> 83

atgcaggatt agagcagcag caacggagcc agaatcagtc tcccaatttg atatccagcc 60

ccgcgcctct tccagcgcg cgcattccac tccatggcgc atg tac ccc aac ctc 115  
Met Tyr Pro Asn Leu  
1 5

ttc cgc acc gca acg gct cac gaa gaa ggc gaa tac atc atc act ggc 163  
Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu Tyr Ile Ile Thr Gly  
10 15 20

gat gaa tca gcc gat gaa atc gca gcc ctg ggc ctc gcc gaa cgt gcc 211  
Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly Leu Ala Glu Arg Ala  
25 30 35

gca ggc tcc acg ctt ggt gaa cgt aaa ttt gct gtc aac acc gtg gaa 259  
Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala Val Asn Thr Val Glu  
40 45 50

ttc cac ggc aac aac ggc cac gtc acc gga ctc acc ggc aac caa atc 307  
Phe His Gly Asn Asn Gly His Val Thr Gly Leu Thr Gly Asn Gln Ile  
55 60 65

cga gtt gtc aac ggc aaa cgt gaa cca atc gaa ggc acc gaa ttc ccc 355  
Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu Gly Thr Glu Phe Pro  
70 75 80 85

ttc gaa gca gac ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa 403  
Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu  
90 95 100

caa ggc gga ttg gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc 451  
Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly  
105 110 115

cgc atc ctc cgc gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt 499  
Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val  
120 125 130

tac atc gca ggc gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca 547  
Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala  
135 140 145

atc gcc gaa ggc cgc gca tgc gcc gca gct atc gac gcc gat ctc atg 595  
Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met  
150 155 160 165

ggt gaa act gca ctc cct gta gca gtt gca cca cag gac gtg ccg ctg 643  
Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu  
170 175 180

gct gtc tagcttgggt agaaaatgct aga 672  
Ala Val

&lt;210&gt; 84

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 84

Met Tyr Pro Asn Leu Phe Arg Thr Ala Thr Ala His Glu Glu Gly Glu  
1 5 10 15

Tyr Ile Ile Thr Gly Asp Glu Ser Ala Asp Glu Ile Ala Ala Leu Gly  
20 25 30

Leu Ala Glu Arg Ala Ala Gly Ser Thr Leu Gly Glu Arg Lys Phe Ala  
35 40 45

Val Asn Thr Val Glu Phe His Gly Asn Asn Gly His Val Thr Gly Leu

50                      55                      60  
 Thr Gly Asn Gln Ile Arg Val Val Asn Gly Lys Arg Glu Pro Ile Glu  
 65                      70                      75                      80  
 Gly Thr Glu Phe Pro Phe Glu Ala Asp Leu Val Leu Val Ala Leu Gly  
 85                      90                      95  
 Phe Thr Gly Ala Glu Gln Gly Gly Leu Ala His Glu Leu Gly Val Gly  
 100                      105                      110  
 Phe Asp Asp Arg Gly Arg Ile Leu Arg Asp Ser Glu Tyr Arg Ser Pro  
 115                      120                      125  
 Thr Asn Ser Arg Val Tyr Ile Ala Gly Asp Asn Gly Arg Gly Gln Ser  
 130                      135                      140  
 Leu Ile Val Trp Ala Ile Ala Glu Gly Arg Ala Cys Ala Ala Ala Ile  
 145                      150                      155                      160  
 Asp Ala Asp Leu Met Gly Glu Thr Ala Leu Pro Val Ala Val Ala Pro  
 165                      170                      175  
 Gln Asp Val Pro Leu Ala Val  
 180

<210> 85  
 <211> 305  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(282)  
 <223> FRXA00198

<400> 85  
 ctc gtt ctt gtt gca ctt ggc ttc acc ggc gca gaa caa ggc gga ttg 48  
 Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu  
 1                      5                      10                      15  
 gca cac gaa cta ggc gta ggt ttc gac gac cgg ggc cgc atc ctc cgc 96  
 Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg  
 20                      25                      30  
 gat tcc gaa tac cgc agc ccc acc aac tcc cgc gtt tac atc gca ggc 144  
 Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly  
 35                      40                      45  
 gac aac ggc cgt ggc cag tcc ctg atc gtg tgg gca atc gcc gaa ggc 192  
 Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly  
 50                      55                      60  
 cgc gca tgc gcc gca gct atc gac gcc gat ctc atg ggt gaa act gca 240  
 Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala  
 65                      70                      75                      80  
 ctc cct gta gca gtt gca cca cag gac gtg ccg ctg gct gtc 282  
 Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val  
 85                      90

tagcttggtt agaaaatgct aga

305

&lt;210&gt; 86

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 86

Leu Val Leu Val Ala Leu Gly Phe Thr Gly Ala Glu Gln Gly Gly Leu  
 1 5 10 15

Ala His Glu Leu Gly Val Gly Phe Asp Asp Arg Gly Arg Ile Leu Arg  
 20 25 30

Asp Ser Glu Tyr Arg Ser Pro Thr Asn Ser Arg Val Tyr Ile Ala Gly  
 35 40 45

Asp Asn Gly Arg Gly Gln Ser Leu Ile Val Trp Ala Ile Ala Glu Gly  
 50 55 60

Arg Ala Cys Ala Ala Ala Ile Asp Ala Asp Leu Met Gly Glu Thr Ala  
 65 70 75 80

Leu Pro Val Ala Val Ala Pro Gln Asp Val Pro Leu Ala Val  
 85 90

&lt;210&gt; 87

&lt;211&gt; 727

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(727)

&lt;223&gt; RXN00365

&lt;400&gt; 87

gaagcctacg atcgcttgca cgcgaccaac aatttccccg agttcaccgg ccgtttgtgc 60

cccgcacctt gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115  
 Met Ile Leu Ser Pro  
 1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163  
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly  
 10 15 20

tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211  
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala  
 25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259  
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr  
 40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc gcc 307  
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly  
 55 60 65

ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355  
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp  
 70 75 80 85  
 atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag 403  
 Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln  
 90 95 100  
 gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc 451  
 Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile  
 105 110 115  
 ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc 499  
 Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly  
 120 125 130  
 cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa 547  
 His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln  
 135 140 145  
 aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa 595  
 Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys  
 150 155 160 165  
 ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc 643  
 Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys  
 170 175 180  
 ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat 691  
 Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp  
 185 190 195  
 atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc 727  
 Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser  
 200 205

&lt;210&gt; 88

&lt;211&gt; 209

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 88

Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys  
 1 5 10 15  
 Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr  
 20 25 30  
 Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala  
 35 40 45  
 Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg  
 50 55 60  
 Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys  
 65 70 75 80  
 Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu  
 85 90 95

Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala  
 100 105 110

Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu  
 115 120 125

Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp  
 130 135 140

Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser  
 145 150 155 160

Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp  
 165 170 175

Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser  
 180 185 190

Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp  
 195 200 205

Ser

<210> 89  
 <211> 727  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(727)  
 <223> FRXA00365

<400> 89  
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cccgccacct gcgaaggcgc ctgcgtgctc ggtatcaacg atg att ctg tca cca 115  
 Met Ile Leu Ser Pro  
 1 5

tca aaa acg ttt gag ctg gaa atc gtc gaa aaa gca ttc cgc gaa ggc 163  
 Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys Ala Phe Arg Glu Gly  
 10 15 20

tgg gtg caa cca gta atc cca tcc atg tct acc ggg ctg tca gtc gcc 211  
 Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr Gly Leu Ser Val Ala  
 25 30 35

gtc gtc ggt tcc ggc ccc gct ggc ctt gcc gcc gcg cag cag ctc acc 259  
 Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala Ala Gln Gln Leu Thr  
 40 45 50

cgc gca ggc cac agc gtt acc gtc ttt gaa cgc gac gac cgc ctc ggc 307  
 Arg Ala Gly His Ser Val Thr Val Phe Glu Arg Asp Asp Arg Leu Gly  
 55 60 65

ggc ctc atg cgc tac ggc gtg cca gaa tac aaa atg gag aac cgc tgg 355  
 Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys Met Glu Asn Arg Trp

70	75	80	85	
atc gac cgc cgc atc gag caa atg gaa gca gag ggc aca act ttc cag				403
Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu Gly Thr Thr Phe Gln	90	95	100	
gta ggc acc tcg ccg cgc gcc gct gaa cta gcg ctt ttc gac gcg atc				451
Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala Leu Phe Asp Ala Ile	105	110	115	
ctc ctc gca acc ggc acc cca gtg gcc cgc gaa ctc tca gtt cca ggc				499
Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu Leu Ser Val Pro Gly	120	125	130	
cac gat ctc aac ggc atc cat gcg gca atg gat tac ctc acc gcc caa				547
His Asp Leu Asn Gly Ile His Ala Ala Met Asp Tyr Leu Thr Ala Gln	135	140	145	
aac cgc atc aac gaa ggc gac ggt gaa gtc tct cca atc aac gcc aaa				595
Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser Pro Ile Asn Ala Lys	150	155	160	165
ggc aag aaa gtt gtc atc atc ggt ggc ggc gac acc ggc acc gac tgc				643
Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp Thr Gly Thr Asp Cys	170	175	180	
ttc ggc acc gca ctg cgc caa gga gca gaa tca gtc acc caa ttt gat				691
Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser Val Thr Gln Phe Asp	185	190	195	
atc cgc ccc cgc gct cct ttc cag cgc gcc gat tcc				727
Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp Ser	200	205		

&lt;210&gt; 90

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 90

Met Ile Leu Ser Pro Ser Lys Thr Phe Glu Leu Glu Ile Val Glu Lys

1	5	10	15
Ala Phe Arg Glu Gly Trp Val Gln Pro Val Ile Pro Ser Met Ser Thr	20	25	30
Gly Leu Ser Val Ala Val Val Gly Ser Gly Pro Ala Gly Leu Ala Ala	35	40	45
Ala Gln Gln Leu Thr Arg Ala Gly His Ser Val Thr Val Phe Glu Arg	50	55	60
Asp Asp Arg Leu Gly Gly Leu Met Arg Tyr Gly Val Pro Glu Tyr Lys	65	70	75
Met Glu Asn Arg Trp Ile Asp Arg Arg Ile Glu Gln Met Glu Ala Glu	85	90	95
Gly Thr Thr Phe Gln Val Gly Thr Ser Pro Arg Ala Ala Glu Leu Ala	100	105	110

Leu Phe Asp Ala Ile Leu Leu Ala Thr Gly Thr Pro Val Ala Arg Glu  
 115 120 125

Leu Ser Val Pro Gly His Asp Leu Asn Gly Ile His Ala Ala Met Asp  
 130 135 140

Tyr Leu Thr Ala Gln Asn Arg Ile Asn Glu Gly Asp Gly Glu Val Ser  
 145 150 155 160

Pro Ile Asn Ala Lys Gly Lys Lys Val Val Ile Ile Gly Gly Gly Asp  
 165 170 175

Thr Gly Thr Asp Cys Phe Gly Thr Ala Leu Arg Gln Gly Ala Glu Ser  
 180 185 190

Val Thr Gln Phe Asp Ile Arg Pro Arg Ala Pro Phe Gln Arg Ala Asp  
 195 200 205

Ser

<210> 91

<211> 480

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(457)

<223> RXA00366

<400> 91

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gccaagaccc agcaatcaag atcatggagg cagtgaagcta atg gcc gac cca caa 115  
 Met Ala Asp Pro Gln  
 1 5

gga ttc atc aaa tac tcc cga cgc gag cct gca cac cgc ccg gtc ccg 163  
 Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala His Arg Pro Val Pro  
 10 15 20

ctg cgc ctc atg gac cac tcc gag gtc tac gaa aag gca ccg gca ggt 211  
 Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu Lys Ala Pro Ala Gly  
 25 30 35

cag atc gag gaa cag gct gcc cgc tgc atg gat tgc ggt gtc ccg ttc 259  
 Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp Cys Gly Val Pro Phe  
 40 45 50

tgc cac gaa ggc tgc cca ctg ggc aac atc atc cct gag tgg aat gat 307  
 Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile Pro Glu Trp Asn Asp  
 55 60 65

ctg gta cgc caa ggt cgg tgg aag gaa gcc tac gat cgc ttg cac gcg 355  
 Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr Asp Arg Leu His Ala  
 70 75 80 85

acc aac aat ttc ccc gag ttc acc ggc cgt ttg tgc ccc gca ccc tgc 403

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<400> 92
Met Ala Asp Pro Gln Gly Phe Ile Lys Tyr Ser Arg Arg Glu Pro Ala
  1          5          10          15

His Arg Pro Val Pro Leu Arg Leu Met Asp His Ser Glu Val Tyr Glu
          20          25          30

Lys Ala Pro Ala Gly Gln Ile Glu Glu Gln Ala Ala Arg Cys Met Asp
          35          40          45

Cys Gly Val Pro Phe Cys His Glu Gly Cys Pro Leu Gly Asn Ile Ile
  50          55          60

Pro Glu Trp Asn Asp Leu Val Arg Gln Gly Arg Trp Lys Glu Ala Tyr
  65          70          75          80

Asp Arg Leu His Ala Thr Asn Asn Phe Pro Glu Phe Thr Gly Arg Leu
          85          90          95

Cys Pro Ala Pro Cys Glu Gly Ala Cys Val Leu Gly Ile Asn Asp Asp
          100          105          110

Ser Val Thr Ile Lys Asn Val
      115

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<400> 93
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aatcgtgctgc gcatgcagcc gagatgggaa cgaggaaatc atg aca gtt gat gag 115
                                         Met Thr Val Asp Glu
                                         1             5

cag gtc tct aac tat tac gac atg ctt ctg aag cgc aat gct ggc gag 163

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Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys Arg Asn Ala Gly Glu	
10 15 20	
cct gaa ttt cac cag gca gtg gca gag gtt ttg gaa tct ttg aag atc	211
Pro Glu Phe His Gln Ala Val Ala Glu Val Leu Glu Ser Leu Lys Ile	
25 30 35	
gtc ctg gaa aag gac cct cat tac gct gat tac ggt ctc atc cag cgc	259
Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr Gly Leu Ile Gln Arg	
40 45 50	
ctg tgc gag cct gag cgt cag ctc atc ttc cgt gtg cct tgg gtt gat	307
Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg Val Pro Trp Val Asp	
55 60 65	
gac cag ggc cag gtc cac gtc aac cgt ggt ttc cgc gtg cag ttc aac	355
Asp Gln Gly Gln Val His Val Asn Arg Gly Phe Arg Val Gln Phe Asn	
70 75 80 85	
tct gca ctt gga cca tac aag ggc ggc ctg cgc ttc cac cca tct gta	403
Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val	
90 95 100	
aac ctg ggc att gtg aag ttc ctg ggc ttt gag cag atc ttt aaa aac	451
Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn	
105 110 115	
tcc cta acc ggc ctg cca atc ggt ggt ggc aag ggt gga tcc gac ttc	499
Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys Gly Gly Ser Asp Phe	
120 125 130	
gac cct aag ggc aag tcc gat ctg gaa atc atg cgt ttc tgc cag tcc	547
Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met Arg Phe Cys Gln Ser	
135 140 145	
ttc atg acc gag ctg cac cgc cac atc ggt gag tac cgc gac gtt cct	595
Phe Met Thr Glu Leu His Arg His Ile Gly Glu Tyr Arg Asp Val Pro	
150 155 160 165	
gca ggt aac atc gga gtt ggt ggc cac gag atc ggt tac ctg ttt ggc	643
Ala Gly Asn Ile Gly Val Gly Gly His Glu Ile Gly Tyr Leu Phe Gly	
170 175 180	
cac tac cgt cgc atg gct aac cag cac gag tcc ggc gtt ttg acc ggt	691
His Tyr Arg Arg Met Ala Asn Gln His Glu Ser Gly Val Leu Thr Gly	
185 190 195	
aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc acc gag gca act ggc	739
Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg Thr Glu Ala Thr Gly	
200 205 210	
tac ggc tgc gtt tac ttc gtg agt gaa atg atc aag gct aag ggc gag	787
Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile Lys Ala Lys Gly Glu	
215 220 225	
agc atc agc ggc cag aag atc atc gtt tcc ggt tcc ggc aac gta gca	835
Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly Ser Gly Asn Val Ala	
230 235 240 245	
acc tac gcg att gaa aag gct cag gaa ctc ggc gca acc gtt att ggt	883
Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly Ala Thr Val Ile Gly	

250	255	260	
ttc tcc gat tcc agc ggt tgg gtt cat acc cct aac ggc gtt gac gtg			931
Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro Asn Gly Val Asp Val			
265	270	275	
gct aag ctc cgc gaa atc aag gaa gtt cgt cgc gca cgc gta tcc gtg			979
Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg Ala Arg Val Ser Val			
280	285	290	
tac gcc gac gaa gtt gaa ggc gca acc tac cac acc gac ggt tcc atc			
1027			
Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His Thr Asp Gly Ser Ile			
295	300	305	
tgg gat ctc aag tgc gat atc gct ctt cct tgt gca act cag aac gag			
1075			
Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu			
310	315	320	325
ctc aac ggc gag aac gct aag act ctt gca gac aac ggc tgc cgt ttc			
1123			
Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp Asn Gly Cys Arg Phe			
330	335	340	
gtt gct gaa ggc gcg aac atg cct tcc acc cct gag gct gtt gag gtc			
1171			
Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro Glu Ala Val Glu Val			
345	350	355	
ttc cgt gag cgc gac atc cgc ttc gga cca ggc aag gca gct aac gct			
1219			
Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly Lys Ala Ala Asn Ala			
360	365	370	
ggt ggc gtt gca acc tcc gct ctg gag atg cag cag aac gct tcg cgc			
1267			
Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln Gln Asn Ala Ser Arg			
375	380	385	
gat tcc tgg agc ttc gag tac acc gac gag cgc ctc cag gtg atc atg			
1315			
Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg Leu Gln Val Ile Met			
390	395	400	405
aag aac atc ttc aag acc tgt gca gag acc gca gca gag tat gga cac			
1363			
Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala Ala Glu Tyr Gly His			
410	415	420	
gag aac gat tac gtt gtc ggc gct aac att gct ggc ttc aag aag gta			
1411			
Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala Gly Phe Lys Lys Val			
425	430	435	
gct gac gcg atg ctg gca cag ggc gtc atc taagaccct gcgctttact			
1461			
Ala Asp Ala Met Leu Ala Gln Gly Val Ile			
440	445		

taa  
1464

<210> 94  
<211> 447  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 94  
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20 25 30  
Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr  
35 40 45  
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg  
50 55 60  
Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe  
65 70 75 80  
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg  
85 90 95  
Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu  
100 105 110  
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys  
115 120 125  
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met  
130 135 140  
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu  
145 150 155 160  
Tyr Arg Asp Val Pro Ala Gly Asn Ile Gly Val Gly Gly His Glu Ile  
165 170 175  
Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser  
180 185 190  
Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg  
195 200 205  
Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile  
210 215 220  
Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly  
225 230 235 240  
Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly  
245 250 255  
Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro  
260 265 270

Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg  
275 280 285

Ala Arg Val Ser Val Tyr Ala Asp Glu Val Glu Gly Ala Thr Tyr His  
290 295 300

Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys  
305 310 315 320

Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp  
325 330 335

Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro  
340 345 350

Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly  
355 360 365

Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln  
370 375 380

Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg  
385 390 395 400

Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala  
405 410 415

Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala  
420 425 430

Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile  
435 440 445

<210> 95

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RAA00525

<400> 95

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atgcgcagtc gatgtcccat cgctgcgtag attagttttc atg aac agc gaa cag 115  
Met Asn Ser Glu Gln  
1 5

gaa ttt gta ctc agc gcc att gaa gaa cgc gac att aag ttt gtg cgt 163  
Glu Phe Val Leu Ser Ala Ile Glu Glu Arg Asp Ile Lys Phe Val Arg  
10 15 20

cta tgg ttc act gac att ctt ggc cac ttg aag tca gtg gtt gtg gct 211  
Leu Trp Phe Thr Asp Ile Leu Gly His Leu Lys Ser Val Val Val Ala  
25 30 35

cct gca gaa cta gag tct gcg ttg gaa gaa ggc atc gga ttc gat ggc 259  
Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly Ile Gly Phe Asp Gly

40	45	50	
tca gcc att gag ggc tac gcg cgt atc tcg gaa gcg gac acc att gcc			307
Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu Ala Asp Thr Ile Ala			
55	60	65	
cgc cca gat cca tcg aca ttc cag gtc ctc cca cta gaa gcg ggc atc			355
Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro Leu Glu Ala Gly Ile			
70	75	80	85
tca aaa ctg cag gca gca cgc ctg ttt tgc gat gtc acg atg cca gac			403
Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp Val Thr Met Pro Asp			
90	95	100	
gga cag cca tct ttt tct gac ccg cgc caa gtg ctg cgc agg cag gtc			451
Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val Leu Arg Arg Gln Val			
105	110	115	
caa cta gct gca gat gaa ggc ttg acc tgc atg atc tca cca gag att			499
Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met Ile Ser Pro Glu Ile			
120	125	130	
gag ttc tat ttg gtg caa agc ctt cgc acc aac gga ctg cca cct gtg			547
Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn Gly Leu Pro Pro Val			
135	140	145	
ccc act gac aac ggc gga tat ttc gac caa gcc aca ttc aat gag gcg			595
Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala Thr Phe Asn Glu Ala			
150	155	160	165
ccg aat ttc cgt cga aac gcg atg gta gcg ctg gag gaa ctc ggc atc			643
Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu Glu Glu Leu Gly Ile			
170	175	180	
cct gtc gag ttc tcc cac cat gaa act gca cct ggc cag caa gaa atc			691
Pro Val Glu Phe Ser His His Glu Thr Ala Pro Gly Gln Gln Glu Ile			
185	190	195	
gat tta cgc cat gcg gat gcg ctc acc atg gcc gac aac atc atg acc			739
Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala Asp Asn Ile Met Thr			
200	205	210	
ttc cgc tac atc atg aaa cag gtg gca agg gac caa ggc gtc ggg gca			787
Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp Gln Gly Val Gly Ala			
215	220	225	
tca ttt atg ccc aag cca ttc caa gaa cat gca ggc tcc gcc atg cac			835
Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala Gly Ser Ala Met His			
230	235	240	245
acg cac atg tcc tta ttt gag ggc gat acc aac gcg ttc cac gat cca			883
Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn Ala Phe His Asp Pro			
250	255	260	
gac gat tct tac atg ctg tcc aaa acc gca aaa cag ttc atc gct gga			931
Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys Gln Phe Ile Ala Gly			
265	270	275	
atc ttg cat cac gct cca gaa ttc acc gct gtg acc aac cag tgg gtc			979
Ile Leu His His Ala Pro Glu Phe Thr Ala Val Thr Asn Gln Trp Val			
280	285	290	

aat tcc tac aaa cgc atc gtg tac gga aac gaa gct cca act gcg gca  
1027

Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu Ala Pro Thr Ala Ala  
295 300 305

acc tgg ggt gta tct aat cgt tct gcg ctg gtt cgt gtt cct acc tac  
1075

Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val Arg Val Pro Thr Tyr  
310 315 320 325

cgt ttg aat aag gag gag tcg cgc cgg gtg gag gtg cgt ctt cct gat  
1123

Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu Val Arg Leu Pro Asp  
330 335 340

acc gct tgt aac cca tat ttg gcg ttt tca gtg atg ctc ggc gct ggt  
1171

Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val Met Leu Gly Ala Gly  
345 350 355

ttg aaa ggc att aaa gaa ggt tat gag ctc gac gag cca gct gag gac  
1219

Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp Glu Pro Ala Glu Asp  
360 365 370

gat atc tcc aac ttg agc ttc cgg gaa cgt cgc gcc atg ggc tac aac  
1267

Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg Ala Met Gly Tyr Asn  
375 380 385

gat ctg cca agc agc ctt gat cag gca ctg cgc caa atg gaa aag tca  
1315

Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg Gln Met Glu Lys Ser  
390 395 400 405

gag ctt gtt gct gac atc ctc ggt gag cac gtt ttt gag ttt ttc ttg  
1363

Glu Leu Val Ala Asp Ile Leu Gly Glu His Val Phe Glu Phe Phe Leu  
410 415 420

cgc aat aag tgg cgt gaa tgg cgt gac tac caa gag cag atc act ccg  
1411

Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln Glu Gln Ile Thr Pro  
425 430 435

tgg gag ctc cga aac aat ctt gat tac tagacttttg cactccaatg  
1458

Trp Glu Leu Arg Asn Asn Leu Asp Tyr  
440 445

gaa  
1461

<210> 96

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

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 20 25 30  
 Ser Val Val Val Ala Pro Ala Glu Leu Glu Ser Ala Leu Glu Glu Gly  
 35 40 45  
 Ile Gly Phe Asp Gly Ser Ala Ile Glu Gly Tyr Ala Arg Ile Ser Glu  
 50 55 60  
 Ala Asp Thr Ile Ala Arg Pro Asp Pro Ser Thr Phe Gln Val Leu Pro  
 65 70 75 80  
 Leu Glu Ala Gly Ile Ser Lys Leu Gln Ala Ala Arg Leu Phe Cys Asp  
 85 90 95  
 Val Thr Met Pro Asp Gly Gln Pro Ser Phe Ser Asp Pro Arg Gln Val  
 100 105 110  
 Leu Arg Arg Gln Val Gln Leu Ala Ala Asp Glu Gly Leu Thr Cys Met  
 115 120 125  
 Ile Ser Pro Glu Ile Glu Phe Tyr Leu Val Gln Ser Leu Arg Thr Asn  
 130 135 140  
 Gly Leu Pro Pro Val Pro Thr Asp Asn Gly Gly Tyr Phe Asp Gln Ala  
 145 150 155 160  
 Thr Phe Asn Glu Ala Pro Asn Phe Arg Arg Asn Ala Met Val Ala Leu  
 165 170 175  
 Glu Glu Leu Gly Ile Pro Val Glu Phe Ser His His Glu Thr Ala Pro  
 180 185 190  
 Gly Gln Gln Glu Ile Asp Leu Arg His Ala Asp Ala Leu Thr Met Ala  
 195 200 205  
 Asp Asn Ile Met Thr Phe Arg Tyr Ile Met Lys Gln Val Ala Arg Asp  
 210 215 220  
 Gln Gly Val Gly Ala Ser Phe Met Pro Lys Pro Phe Gln Glu His Ala  
 225 230 235 240  
 Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Thr Asn  
 245 250 255  
 Ala Phe His Asp Pro Asp Asp Ser Tyr Met Leu Ser Lys Thr Ala Lys  
 260 265 270  
 Gln Phe Ile Ala Gly Ile Leu His His Ala Pro Glu Phe Thr Ala Val  
 275 280 285  
 Thr Asn Gln Trp Val Asn Ser Tyr Lys Arg Ile Val Tyr Gly Asn Glu  
 290 295 300  
 Ala Pro Thr Ala Ala Thr Trp Gly Val Ser Asn Arg Ser Ala Leu Val  
 305 310 315 320  
 Arg Val Pro Thr Tyr Arg Leu Asn Lys Glu Glu Ser Arg Arg Val Glu

	325		330		335
Val Arg Leu Pro Asp Thr Ala Cys Asn Pro Tyr Leu Ala Phe Ser Val					
	340		345		350
Met Leu Gly Ala Gly Leu Lys Gly Ile Lys Glu Gly Tyr Glu Leu Asp					
	355		360		365
Glu Pro Ala Glu Asp Asp Ile Ser Asn Leu Ser Phe Arg Glu Arg Arg					
	370		375		380
Ala Met Gly Tyr Asn Asp Leu Pro Ser Ser Leu Asp Gln Ala Leu Arg					
	385		390		395
Gln Met Glu Lys Ser Glu Leu Val Ala Asp Ile Leu Gly Glu His Val					
	405		410		415
Phe Glu Phe Phe Leu Arg Asn Lys Trp Arg Glu Trp Arg Asp Tyr Gln					
	420		425		430
Glu Gln Ile Thr Pro Trp Glu Leu Arg Asn Asn Leu Asp Tyr					
	435		440		445

&lt;210&gt; 97

&lt;211&gt; 1554

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1531)

&lt;223&gt; RXA00335

&lt;400&gt; 97

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tacaaataaa ccgttccgcc catgtcaatg aggagtcacc gtg gcg ttt gaa acc	115
Val Ala Phe Glu Thr	
1 5	

ccg gaa gaa att gtc aag ttc atc aag gat gaa aac gtc gag ttc gtt	163
Pro Glu Glu Ile Val Lys Phe Ile Lys Asp Glu Asn Val Glu Phe Val	
10 15 20	

gac gtt cga ttc acc gac ctt ccc ggc acc gag cag cac ttc agc atc	211
Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu Gln His Phe Ser Ile	
25 30 35	

cca gct gcc agc ttc gat gca gat aca atc gaa gaa ggt ctc gca ttc	259
Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu Glu Gly Leu Ala Phe	
40 45 50	

gac gga tcc tcg atc cgt ggc ttc acc acg atc gac gaa tct gac atg	307
Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile Asp Glu Ser Asp Met	
55 60 65	

aat ctc ctg cca gac ctc gga acg gcc acc ctt gat cca ttc cgc aag	355
Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu Asp Pro Phe Arg Lys	
70 75 80 85	

gca aag acc ctg aac gtt aag ttc ttc gtt cac gat cct ttc acc cgc 403  
 Ala Lys Thr Leu Asn Val Lys Phe Phe Val His Asp Pro Phe Thr Arg  
 90 95 100

gag gca ttc tcc cgc gac cca cgc aac gtg gca cgc aag gca gag cag 451  
 Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala Arg Lys Ala Glu Gln  
 105 110 115

tac ctg gca tcc acc ggc att gca gac acc tgc aac ttc ggc gcc gag 499  
 Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys Asn Phe Gly Ala Glu  
 120 125 130

gct gag ttc tac ctc ttc gac tcc gtt cgc tac tcc acc gag atg aac 547  
 Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr Ser Thr Glu Met Asn  
 135 140 145

tcc ggc ttc tac gaa gta gat acc gaa gaa ggc tgg tgg aac cgt ggc 595  
 Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly Trp Trp Asn Arg Gly  
 150 155 160 165

aag gaa acc aac ctc gac ggc acc cca aac ctg ggc gca aag aac cgc 643  
 Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu Gly Ala Lys Asn Arg  
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gtc aag ggt ggc tac ttc cca gta gca cca tac gac caa acc gtt gac 691  
 Val Lys Gly Tyr Phe Pro Val Ala Pro Tyr Asp Gln Thr Val Asp  
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 Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala Ser Gly Phe Ala Leu  
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gag cgt ttc cac cac gaa gtc ggt ggc gga cag cag gaa atc aac tac 787  
 Glu Arg Phe His His Glu Val Gly Gly Gly Gln Gln Glu Ile Asn Tyr  
 215 220 225

cgc ttc aac acc atg ctc cac gcg gca gat gat atc cag acc ttc aag 835  
 Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp Ile Gln Thr Phe Lys  
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tac atc atc aag aac acc gct cgc ctc cac ggc aag gct gca acc ttc 883  
 Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly Lys Ala Ala Thr Phe  
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atg cct aag cca ctg gct ggc gac aac ggt tcc ggc atg cac gct cac 931  
 Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser Gly Met His Ala His  
 265 270 275

cag tcc ctc tgg aag gac ggc aag cca ctc ttc cac gat gag tcc ggc 979  
 Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe His Asp Glu Ser Gly  
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tac gca ggc ctg tcc gac atc gcc cgc tac tac atc ggc ggc atc ctg  
 1027  
 Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr Ile Gly Gly Ile Leu  
 295 300 305

cac cac gca ggc gct gtt ctg gcg ttc acc aac gca acc ctg aac tcc  
 1075  
 His His Ala Gly Ala Val Leu Ala Phe Thr Asn Ala Thr Leu Asn Ser  
 310 315 320 325

tac cac cgt ctg gtt cca ggc ttc gag gct cca atc aac ctg gtg tac  
1123

Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro Ile Asn Leu Val Tyr  
330 335 340

tca cag cgc aac cgt tcc gct gct gtc cgt atc cca atc acc gga tcc  
1171

Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile Pro Ile Thr Gly Ser  
345 350 355

aac ccg aag gca aag cgc atc gaa ttc cgc gct cca gac cca tca ggc  
1219

Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala Pro Asp Pro Ser Gly  
360 365 370

aac cca tac ctg ggc ttt gca gcg atg atg atg gcc ggc ctc gac ggc  
1267

Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met Ala Gly Leu Asp Gly  
375 380 385

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1315

Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val Asp Lys Asp Leu Tyr  
390 395 400 405

gaa cta cca cca gag gaa gct gca tcc att cca cag gca cca acc tcc  
1363

Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro Gln Ala Pro Thr Ser  
410 415 420

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1411

Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp Thr Asp Phe Leu Thr  
425 430 435

gag tct gac gtc ttc acc gag gat ctc atc gag gcg tac atc cag tac  
1459

Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu Ala Tyr Ile Gln Tyr  
440 445 450

aag tac gac aac gag atc tcc cca gtt cgc ctg cgc cca acc ccg cag  
1507

Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu Arg Pro Thr Pro Gln  
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<213> Corynebacterium glutamicum

<400> 98

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Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Ile Glu  
                   35                                  40                                  45

Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile  
                   50                                  55                                  60

Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu  
                   65                                  70                                  75                                  80

Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His  
                                   85                                  90                                  95

Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala  
                                   100                                  105                                  110

Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys  
                                   115                                  120                                  125

Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr  
                   130                                  135                                  140

Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly  
                   145                                  150                                  155                                  160

Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu  
                                   165                                  170                                  175

Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr  
                                   180                                  185                                  190

Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala  
                   195                                  200                                  205

Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln  
                   210                                  215                                  220

Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp  
                   225                                  230                                  235                                  240

Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly  
                                   245                                  250                                  255

Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser  
                                   260                                  265                                  270

Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe  
                   275                                  280                                  285

His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr  
                   290                                  295                                  300

Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn  
                   305                                  310                                  315                                  320

Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro  
                                   325                                  330                                  335

Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

340	345	350
Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Ile Glu Phe Arg Ala		
355	360	365
Pro Asp Pro Ser Gly Asn Pro Tyr Leu Gly Phe Ala Ala Met Met Met		
370	375	380
Ala Gly Leu Asp Gly Ile Lys Asn Arg Ile Glu Pro His Ala Pro Val		
385	390	395
Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile Pro		
405	410	415
Gln Ala Pro Thr Ser Leu Glu Ala Ser Leu Lys Ala Leu Gln Glu Asp		
420	425	430
Thr Asp Phe Leu Thr Glu Ser Asp Val Phe Thr Glu Asp Leu Ile Glu		
435	440	445
Ala Tyr Ile Gln Tyr Lys Tyr Asp Asn Glu Ile Ser Pro Val Arg Leu		
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&lt;400&gt; 99

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Met Ser Gly Pro Leu	

aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa	163
Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys	
10 15 20	

gtt ggt tct tta tct ctg aaa tct gag cat gcc caa gca gat cta gag	211
Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu	
25 30 35	

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His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu	
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tca ggt gca ggc gat ccc gat gtc gcg ctg aac ctt ctt att cgg ctg	307
Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu	
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tat cag gca ctt gaa gca atc ggc gag gat gct cga aac gag ctt gat	355
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Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala Arg Asn Glu Leu Asp  
 70 75 80 85  
 caa gag att cgc cag gat gaa aaa cta cga gtc cgc ctt ttt gca ttg 403  
 Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val Arg Leu Phe Ala Leu  
 90 95 100  
 ttg ggt ggt tcc tcg gct gtc ggt gat cac ttg gtc gcc aat cct ttg 451  
 Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu Val Ala Asn Pro Leu  
 105 110 115  
 cag tgg aaa ctc tta aaa ctt gat gcg cca tcg agg gaa gag atg ttt 499  
 Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser Arg Glu Glu Met Phe  
 120 125 130  
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 Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro Ala Val Leu Glu Val  
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 gag gat ttc agc gat gca cac aac att gcc cga gac gat ttg agc acg 595  
 Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg Asp Asp Leu Ser Thr  
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 Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro Glu Ala Glu Arg Val  
 170 175 180  
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 Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg Ile Ala Ala His Asp  
 185 190 195  
 tta gcg ggt acc tat ccc acc gac atg cgg aga aaa ggt ggc gat cct 739  
 Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg Lys Gly Gly Asp Pro  
 200 205 210  
 gtt ccg ttt agc aca gtg acc atg cag ctc agc gac cta gct gat gct 787  
 Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser Asp Leu Ala Asp Ala  
 215 220 225  
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 230 235 240 245  
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 Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala Met Gly Lys Cys Gly  
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 gcg cag gaa ttg aac tac att tca gat gtg gac gtg gtg ttt gtt gca 931  
 Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp Val Val Phe Val Ala  
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 Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala Ala Glu Leu Ile Arg  
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 atc ggt agc aac tcg ttc ttt gag gtg gat gca gca ctt cgc cca gaa  
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 Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala Ala Leu Arg Pro Glu  
 295 300 305

ggt aaa agt ggc gct ctt gtg cgc tct ttg gat tcc cat atg gcg tat  
1075

Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp Ser His Met Ala Tyr  
310 315 320 325

tac aag cgc tgg gcg gaa acc tgg gag ttt cag gca ctg ctg aaa gct  
1123

Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala  
330 335 340

cgt ccc atg acg ggt gat att aac ctt ggg cag tcc tat gtg gat gct  
1171

Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala  
345 350 355

ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca  
1219

Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr  
360 365 370

gat gtc caa gct atg cgc cgt cga gtg ttg gac aat gtt ccg gaa gac  
1267

Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp  
375 380 385

ttg cgt gat cgt gag ctg aag ctt ggt cgc ggt ggt ttg agg gat gtg  
1315

Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val  
390 395 400 405

gag ttt gct gtc cag ctc ctt cag atg gtg cat ggt cgc att gat gag  
1363

Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu  
410 415 420

acg ttg cgg gtt cgg tca acg gta aat gct ttg cat gtg ttg gtt gat  
1411

Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp  
425 430 435

cag gga tat gtg ggt cgt gaa gac ggg cat aat ctc att gag tcg tat  
1459

Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr  
440 445 450

gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag  
1507

Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys  
455 460 465

cgc act cac ttg tta ccg aaa cct gat gac cga atg aat atg cgc tgg  
1555

Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg Met Asn Met Arg Trp  
470 475 480 485

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1603

Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala  
490 495 500

aaa gct atg gaa cgg cat ttg cgt aag gtt cgt ttg cag att cag tcg  
1651

Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser  
505 510 515

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1699

Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn  
520 525 530

ttg agc gcg gat gcc atc agg ttg tct ccg gat gct gca aag cta caa  
1747

Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln  
535 540 545

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1795

Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu  
550 555 560 565

act gct ctt gca tca gga gct agc cgt aaa gcc aag att cag gcg atg  
1843

Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met  
570 575 580

ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat  
1891

Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp  
585 590 595

gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc  
1939

Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg  
600 605 610

agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg  
1987

Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg  
615 620 625

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2035

Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile  
630 635 640 645

tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct  
2083

Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro  
650 655 660

aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca  
2131

Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala  
665 670 675

acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga  
2179

Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg  
680 685 690

tcg ctg agg agg cag gag ctg gca cgc att gcc tct gct gat ttg ctc  
2227

Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu  
695 700 705

aac atg ctc act gtt cag gaa gta tgc caa agc ttg tca cta gtc tgg  
2275

Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp  
710 715 720 725

gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt  
2323

Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu  
730 735 740

aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc  
2371

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2419

Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala  
760 765 770

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2467

Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu  
775 780 785

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Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg  
810 815 820

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2611

Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val  
825 830 835

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2659

Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu  
840 845 850

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2707

Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu  
855 860 865

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Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala  
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2803

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890 895 900

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2851

Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly  
905 910 915

gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat  
2899

Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His  
920 925 930

gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt  
2947

Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu  
935 940 945

gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg  
2995

Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr  
950 955 960 965

ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg  
3043

Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala Arg Asn Ala Leu Val  
970 975 980

ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac  
3091

Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro Thr Pro Gly Pro His  
985 990 995

ctt gcg cag gtg gct ggt gcg tct ggt tgg gat cca aat gag tac cag  
3139

Leu Ala Gln Val Ala Gly Ala Ser Gly Trp Asp Pro Asn Glu Tyr Gln  
1000 1005 1010

gag tat ttg gaa aac tat ctg aaa gtg acc agg aag agt cgt cag gtt  
3187

Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val  
1015 1020 1025

gtt gat gaa gtc ttc tgg ggt gtg gac tct atg gag caa cgt gag ttt  
3235

Val Asp Glu Val Phe Trp Gly Val Asp Ser Met Glu Gln Arg Glu Phe  
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3258

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<213> Corynebacterium glutamicum

<400> 100

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Gln Ala Asp Leu Glu His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp	35	40	45
Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn	50	55	60
Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala	65	70	75
Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val	85	90	95
Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu	100	105	110
Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser	115	120	125
Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro	130	135	140
Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg	145	150	155
Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro	165	170	175
Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg	180	185	190
Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg	195	200	205
Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser	210	215	220
Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala	225	230	235
Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala	245	250	255
Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp	260	265	270
Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala	275	280	285
Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala	290	295	300
Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp	305	310	315
Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln	325	330	335

Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln  
 340 345 350  
 Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg  
 355 360 365  
 Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp  
 370 375 380  
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly  
 385 390 395 400  
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His  
 405 410 415  
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu  
 420 425 430  
 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn  
 435 440 445  
 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln  
 450 455 460  
 Leu Glu Arg Ile Lys Arg Thr His Leu Leu Pro Lys Pro Asp Asp Arg  
 465 470 475 480  
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met  
 485 490 495  
 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg  
 500 505 510  
 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu  
 515 520 525  
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp  
 530 535 540  
 Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg  
 545 550 555 560  
 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala  
 565 570 575  
 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln  
 580 585 590  
 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp  
 595 600 605  
 Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly  
 610 615 620  
 Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile  
 625 630 635 640  
 Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp  
 645 650 655

Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val  
 660 665 670  
 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala  
 675 680 685  
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala  
 690 695 700  
 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser  
 705 710 715 720  
 Leu Ser Leu Val Trp Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu  
 725 730 735  
 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala  
 740 745 750  
 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly  
 755 760 765  
 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly  
 770 775 780  
 Val Glu Glu His Glu Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser  
 785 790 795 800  
 Met Arg Ser Arg Leu Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val  
 805 810 815  
 Asp Leu Gly Leu Arg Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr  
 820 825 830  
 Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu  
 835 840 845  
 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu  
 850 855 860  
 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp  
 865 870 875 880  
 Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg  
 885 890 895  
 Val Asp Asn Glu Arg Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr  
 900 905 910  
 Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu  
 915 920 925  
 Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser  
 930 935 940  
 Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro  
 945 950 955 960  
 Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala  
 965 970 975  
 Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro

[illegible]

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<210> 101
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(861)  
<223> RXN03176
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<400> 101																
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Glu	Leu	Ala	Asp	Tyr	Ile	Pro	Glu	Leu	Lys	Ser	Ala	Asp	Pro	Asn	Pro	
1			5			10			15							
ctg	gca	gta	gcc	ctg	tgc	acc	gtt	aac	gga	cac	atc	tac	agc	gca	ggc	96
Leu	Ala	Val	Ala	Leu	Cys	Thr	Val	Asn	Gly	His	Ile	Tyr	Ser	Ala	Gly	
20			25			30										
gat	gac	gac	atc	gaa	ttc	acc	atg	caa	agt	att	tcc	aag	cca	ttt	gcc	144
Asp	Asp	Asp	Ile	Glu	Phe	Thr	Met	Gln	Ser	Ile	Ser	Lys	Pro	Phe	Ala	
35			40			45										
tac	gca	ctc	gca	ctc	caa	gaa	tgc	ggc	ttt	gat	gag	gtc	tct	gca	tcc	192
Tyr	Ala	Leu	Ala	Leu	Gln	Glu	Cys	Gly	Phe	Asp	Glu	Val	Ser	Ala	Ser	
50			55			60										
gtg	gcc	ttg	gag	ccc	tcc	ggt	gag	gcc	ttc	aac	gaa	ctt	tcc	ctc	gac	240
Val	Ala	Leu	Glu	Pro	Ser	Gly	Glu	Ala	Phe	Asn	Glu	Leu	Ser	Leu	Asp	
65			70			75			80							
ggc	gaa	aac	cgc	ccc	atg	aac	ccc	atg	atc	aac	gcc	ggc	gcg	atc	gcc	288
Gly	Glu	Asn	Arg	Pro	Met	Asn	Pro	Met	Ile	Asn	Ala	Gly	Ala	Ile	Ala	
85			90			95										
atc	aac	cag	ctg	atc	aac	ggc	tcc	gat	tcc	acc	gtg	gaa	gac	cgc	gtg	336
Ile	Asn	Gln	Leu	Ile	Asn	Gly	Ser	Asp	Ser	Thr	Val	Glu	Asp	Arg	Val	
100			105			110										
gaa	aaa	atc	cga	cac	tac	ttc	tct	gaa	ctt	gct	gga	cgc	gaa	ctc	acc	384
Glu	Lys	Ile	Arg	His	Tyr	Phe	Ser	Glu	Leu	Ala	Gly	Arg	Glu	Leu	Thr	
115			120			125										
atc	gac	cgc	gtg	ctt	gcc	gaa	tcc	gaa	ctc	gcc	ggc	gcc	gac	cgc	aac	432
Ile	Asp	Arg	Val	Leu	Ala	Glu	Ser	Glu	Leu	Ala	Gly	Ala	Asp	Arg	Asn	
130			135			140										

ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa 480  
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160

gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta 528  
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175

acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc 576  
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190

aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc 624  
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205

ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg 672  
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220

cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc 720  
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240

gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc 768  
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255

cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816  
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270

aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861  
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

&lt;210&gt; 102

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 102

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro  
 1 5 10 15

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly  
 20 25 30

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala  
 35 40 45

Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser  
 50 55 60

Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp  
 65 70 75 80

Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala  
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val  
 100 105 110

Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr  
 115 120 125

Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn  
 130 135 140

Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160

Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175

Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190

Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205

Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220

Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240

Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255

Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270

Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

&lt;210&gt; 103

&lt;211&gt; 861

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(861)

&lt;223&gt; FRXA02879

&lt;400&gt; 103

gag ttg gcc gat tac atc ccg gaa cta aaa tct gcg gac cca aac ccg 48

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro

1

5

10

15

ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96

Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly

20

25

30

gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144

Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala

35

40

45

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
50 55 60	
gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa	480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu	
145 150 155 160	
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta	528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val	
165 170 175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc	576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly	
180 185 190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc	624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg	
195 200 205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg	672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly	
210 215 220	
cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc	720
Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly	
225 230 235 240	
gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc	768
Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser	
245 250 255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc	816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe	
260 265 270	
aaa cag ctt tcc gac gac atg ggc ctc cgc ctc atc gcc acc gag	861
Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu	
275 280 285	

&lt;210&gt; 104

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 104

Glu Leu Ala Asp Tyr Ile Pro Glu Leu Lys Ser Ala Asp Pro Asn Pro  
 1 5 10 15  
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly  
 20 25 30  
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala  
 35 40 45  
 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser  
 50 55 60  
 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp  
 65 70 75 80  
 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala  
 85 90 95  
 Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val  
 100 105 110  
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr  
 115 120 125  
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn  
 130 135 140  
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu  
 145 150 155 160  
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val  
 165 170 175  
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly  
 180 185 190  
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg  
 195 200 205  
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly  
 210 215 220  
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly  
 225 230 235 240  
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser  
 245 250 255  
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe  
 260 265 270  
 Lys Gln Leu Ser Asp Asp Met Gly Leu His Leu Met Ser Thr Glu  
 275 280 285

<210> 105  
 <211> 1155  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1132)  
 <223> RXA00278

<400> 105  
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 gtgggtcggc atccgcccc gtttgcagga gtacttataa atg cac gct ttt cga 115  
 Met His Ala Phe Arg  
 1 5  
 cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca 163  
 Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala  
 10 15 20  
 acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc 211  
 Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr  
 25 30 35  
 ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct 259  
 Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser  
 40 45 50  
 tcg att gaa gct ccc ggt gaa aaa gag ccc att gtg gaa gta ata gag 307  
 Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu  
 55 60 65  
 aat tgg cca ggt tct tta cgc ccg gat gat ctg acc cct gag gag cgg 355  
 Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg  
 70 75 80 85  
 gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa 403  
 Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln  
 90 95 100  
 tcg caa aac ttg ctc agt ttc cgt gat ccg gtg act ggt gag ctg cgc 451  
 Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg  
 105 110 115  
 ggt ttt gaa gtg gaa tta gcg agg gaa att tcc cgc gac att ttc ggt 499  
 Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly  
 120 125 130  
 gac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg 547  
 Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu  
 135 140 145  
 cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg 595  
 Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr  
 150 155 160 165  
 atc acc gac gaa cgc gcc aaa ttg gtg gaa ttt tcc aca ccg tac ctg 643  
 Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu  
 170 175 180

cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691  
 Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser Ser Gly Ile Thr Ser  
 185 190 195

atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739  
 Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr  
 200 205 210

tca ttg cag cga gcc cgc acc att gcg cgg gag gcc tca atc tta aaa 787  
 Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys  
 215 220 225

act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835  
 Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala  
 230 235 240 245

cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883  
 Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln  
 250 255 260

gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931  
 Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr  
 265 270 275

gga gtg gca gcg gca tcg acc act gct gaa aca gac tct tcg ggg ttg 979  
 Gly Val Ala Ala Ser Thr Thr Ala Glu Thr Asp Ser Ser Gly Leu  
 280 285 290

att cgg cag gta aac tac aca att gaa cgg atc cgc aca gac cgc atg  
 1027  
 Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile Arg Thr Asp Arg Met  
 295 300 305

tgg tgg aca atg ttc gac gat tgg ttc gga cct tat ctc tgg tcc tac  
 1075  
 Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr  
 310 315 320 325

ggt cca cca cag ctg cag tac atg cca gag gaa gaa ggg aca gaa aac  
 1123  
 Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu Glu Gly Thr Glu Asn  
 330 335 340

gat gaa gga taatgaagat ttgatccag att  
 1155  
 Asp Glu Gly

&lt;210&gt; 106

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106

Met His Ala Phe Arg Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala  
 1 5 10 15

Ala Leu Leu Ala Ala Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val  
 20 25 30

Glu Pro Ala Glu Thr Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro  
 35 40 45  
 Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile  
 50 55 60  
 Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu  
 65 70 75 80  
 Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile  
 85 90 95  
 Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val  
 100 105 110  
 Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser  
 115 120 125  
 Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly  
 130 135 140  
 Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val  
 145 150 155 160  
 Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe  
 165 170 175  
 Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser  
 180 185 190  
 Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val  
 195 200 205  
 Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu  
 210 215 220  
 Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu  
 225 230 235 240  
 Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser  
 245 250 255  
 Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu  
 260 265 270  
 Asp Ser His Ser Tyr Gly Val Ala Ala Ala Ser Thr Thr Ala Glu Thr  
 275 280 285  
 Asp Ser Ser Gly Leu Ile Arg Gln Val Asn Tyr Thr Ile Glu Arg Ile  
 290 295 300  
 Arg Thr Asp Arg Met Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro  
 305 310 315 320  
 Tyr Leu Trp Ser Tyr Gly Pro Pro Gln Leu Gln Tyr Met Pro Glu Glu  
 325 330 335  
 Glu Gly Thr Glu Asn Asp Glu Gly  
 340

<210> 107  
 <211> 1035  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1012)  
 <223> RXA00727

<400> 107  
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 ttcgcagaca ccgcctctga aacggctact gcatagcact ttg cgt ttc ccc aaa 115  
 Leu Arg Phe Pro Lys  
 1 5  
 atc ccc aag cgc gct gta gcg gcg acc gtc ggc atc gtg gca acc tca 163  
 Ile Pro Lys Arg Ala Val Ala Ala Thr Val Gly Ile Val Ala Thr Ser  
 10 15 20  
 ttc acc ttg gct tct tgt gtc acc aat gag gag cag ggc aac cca gat 211  
 Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu Gln Gly Asn Pro Asp  
 25 30 35  
 ggc tgg gag cag atc gtt cca gat cct gta ccg gag att cag gcg atg 259  
 Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro Glu Ile Gln Ala Met  
 40 45 50  
 gtt ccc gaa gct ctg gct cag cgc ggt gtg ctc acc gcc ggt gcc aac 307  
 Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu Thr Ala Gly Ala Asn  
 55 60 65  
 cca cct ttc cca ccg ttt gag ttt aaa gat tcc gat ggt cag att atc 355  
 Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser Asp Gly Gln Ile Ile  
 70 75 80 85  
 ggt gtg gaa atg gac ctc gtg cgt gca atg gcg ggg gtg atg ggc ttg 403  
 Gly Val Glu Met Asp Leu Val Arg Ala Met Ala Gly Val Met Gly Leu  
 90 95 100  
 gag ttc agc cct cag gag cag gat ttc tcc ctc atc ctt cca tcg gtt 451  
 Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu Ile Leu Pro Ser Val  
 105 110 115  
 caa gct ggc acc ctt gat atc gga gcc tct ggc ttc act gac aac gag 499  
 Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly Phe Thr Asp Asn Glu  
 120 125 130  
 gaa cgc cgc gag aac ttt gat ttc atc gat ttc ctc ttc gca ggt gtg 547  
 Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe Leu Phe Ala Gly Val  
 135 140 145  
 cag tgg gcg cag gca act gat cgt gaa acc cca atc gat ccg gaa aac 595  
 Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro Ile Asp Pro Glu Asn  
 150 155 160 165  
 gcc tgt ggt ctc acc gtt gct gta cag cgc aca acc gtg gca gag acc 643  
 Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr Thr Val Ala Glu Thr  
 170 175 180

gac gat gtc cgt cct cgc tca gct caa tgt gaa gcc gaa ggc aaa gag 691  
 Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu Ala Glu Gly Lys Glu  
 185 190 195

ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739  
 Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala  
 200 205 210

ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787  
 Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser  
 215 220 225

gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835  
 Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp  
 230 235 240 245

atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883  
 Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp  
 250 255 260

ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931  
 Leu Thr Pro Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly  
 265 270 275

gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979  
 Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu  
 280 285 290

gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa  
 1032  
 Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn  
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 1035

<210> 108

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

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Ile Val Ala Thr Ser Phe Thr Leu Ala Ser Cys Val Thr Asn Glu Glu  
 20 25 30

Gln Gly Asn Pro Asp Gly Trp Glu Gln Ile Val Pro Asp Pro Val Pro  
 35 40 45

Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu  
 50 55 60

Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser  
 65 70 75 80

Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala  
 85 90 95

Gly Val Met Gly Leu Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu  
 100 105 110

Ile Leu Pro Ser Val Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly  
 115 120 125

Phe Thr Asp Asn Glu Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe  
 130 135 140

Leu Phe Ala Gly Val Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro  
 145 150 155 160

Ile Asp Pro Glu Asn Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr  
 165 170 175

Thr Val Ala Glu Thr Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu  
 180 185 190

Ala Glu Gly Lys Glu Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp  
 195 200 205

Thr Ala Ala Thr Ala Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala  
 210 215 220

Asp Ser Pro Val Ser Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile  
 225 230 235 240

Glu Val Val Gly Asp Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe  
 245 250 255

Pro Leu Glu Ser Asp Leu Thr Pro Ala Ala Ala Ala Phe Gln His  
 260 265 270

Leu Ile Asp Thr Gly Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile  
 275 280 285

Glu Glu Gly Leu Leu Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn  
 290 295 300

<210> 109

<211> 1962

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1939)

<223> RXA02139

<400> 109

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tgaagcattc gttcctgcac tcgagcgggc cttgccatgc atg cgc cac cgt ggt 115  
 Met Arg His Arg Gly  
 1 5

cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc 163

Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp Ala Ala Phe Gly Phe	
10 15 20	
aac cgc ctc tcc atc att gat att gca cac tcc cac caa cca ctg cgt	211
Asn Arg Leu Ser Ile Ile Asp Ile Ala His Ser His Gln Pro Leu Arg	
25 30 35	
tgg gga cct gcg gat gaa ccc gac cgc tac gca atg act ttc aac ggt	259
Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala Met Thr Phe Asn Gly	
40 45 50	
gag atc tac aac tac gtt gag ctg cgt aaa gag ctc tcg gat ttg gga	307
Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu Leu Ser Asp Leu Gly	
55 60 65	
tat gcc ttt aat act tct ggc gat ggc gag cca att gtt gtc ggt ttc	355
Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro Ile Val Val Gly Phe	
70 75 80 85	
cac cac tgg ggc gag tcc gtg gtc gag cat ctc cgc gga atg ttc ggc	403
His His Trp Gly Glu Ser Val Val Glu His Leu Arg Gly Met Phe Gly	
90 95 100	
att gcc att tgg gat aca aag gaa aag tcg ctt ttc ctt gcg cgt gat	451
Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu Phe Leu Ala Arg Asp	
105 110 115	
cag ttc ggc att aag cca ctg ttc tac gca acc acc gag cat ggc acc	499
Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr Thr Glu His Gly Thr	
120 125 130	
gtg ttc tcc tca gag aag aag acc atc ttg gag atg gcc gag gag atg	547
Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu Met Ala Glu Glu Met	
135 140 145	
aat cta gat ctg ggc ctt gat aag cgc acc att gag cac tac gtg gac	595
Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile Glu His Tyr Val Asp	
150 155 160 165	
ttg cag tac gtg ccc gag cca gat acc ctt cac gcg cag att tcc cgc	643
Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His Ala Gln Ile Ser Arg	
170 175 180	
ttg gag tca ggc tgc acc gca aca gtt cgt ccg ggc ggc aag ctg gaa	691
Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro Gly Gly Lys Leu Glu	
185 190 195	
cag aag cgt tac ttc aag cct cag ttc cca gta cag aag gtc gta aag	739
Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val Gln Lys Val Val Lys	
200 205 210	
ggt aag gag cag gac ctc ttc gat cgc att gcc cag gtg ttg gag gat	787
Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala Gln Val Leu Glu Asp	
215 220 225	
agc gtc gaa aag cat atg cgt gcc gac gtg acc gta ggc tcg ttc ctt	835
Ser Val Glu Lys His Met Arg Ala Asp Val Thr Val Gly Ser Phe Leu	
230 235 240 245	
ttc ggc ggc att gac tca acc gca att gcg gcg ctt gca aag cgc cac	883
Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala Leu Ala Lys Arg His	

250	255	260	
aac cct gac ctg ctc acc ttc acc acc ggt ttc gag cgt gaa ggc tac			931
Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe Glu Arg Glu Gly Tyr			
265	270	275	
tcg gag gtc gat gtg gct gcg gag tcc gcc gct gcg att ggc gct gag			979
Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala Ala Ile Gly Ala Glu			
280	285	290	
cac atc gtg aag att gtc tcg cct gag gaa tac gcc aac gcg att cct			
1027			
His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr Ala Asn Ala Ile Pro			
295	300	305	
aag atc atg tgg tac ttg gat gat cct gta gct gac cca tca ttg gtc			
1075			
Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala Asp Pro Ser Leu Val			
310	315	320	325
ccg ctg tac ttc gtg gca gcg gaa gca cgt aag cac gtc aag gtt gtg			
1123			
Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys His Val Lys Val Val			
330	335	340	
ctg tct ggc gag ggc gca gat gag ctg ttc ggt gga tac acc att tac			
1171			
Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly Gly Tyr Thr Ile Tyr			
345	350	355	
aag gag ccg cta tcg ctt gct cca ttt gag aag atc cct tcc cca cta			
1219			
Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys Ile Pro Ser Pro Leu			
360	365	370	
cgt aaa ggc ctg gga aag ctc agc aag gtt ctg cca gac ggc atg aag			
1267			
Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu Pro Asp Gly Met Lys			
375	380	385	
ggc aag tcc ctt ctt gag cgt ggc tcc atg acc atg gaa gag cgc tac			
1315			
Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr Met Glu Glu Arg Tyr			
390	395	400	405
tac ggc aac gct cgc tcc ttc aat ttc gag cag atg caa cgc gtt att			
1363			
Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln Met Gln Arg Val Ile			
410	415	420	
cca tgg gca aag cgc gaa tgg gac cac cgc gaa gtc act gcg ccg atc			
1411			
Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu Val Thr Ala Pro Ile			
425	430	435	
tac gca cag tcc cgc aac ttt gat cca gta gcc cgc atg caa cac ctg			
1459			
Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala Arg Met Gln His Leu			
440	445	450	

gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag  
1507

Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys  
455 460 465

atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag  
1555

Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys  
470 475 480 485

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc  
1603

Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala  
490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt  
1651

Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val  
505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg  
1699

Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met  
520 525 530

cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc  
1747

Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr  
535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg  
1795

Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu  
550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga  
1843

Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg  
570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa  
1891

Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu  
585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt  
1939

Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu  
600 605 610

taagtcttaa agcctaaacc ccc  
1962

<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp

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His Gln Pro Leu Arg Trp Gly Pro Ala Asp Glu Pro Asp Arg Tyr Ala			
35	40	45	
Met Thr Phe Asn Gly Glu Ile Tyr Asn Tyr Val Glu Leu Arg Lys Glu			
50	55	60	
Leu Ser Asp Leu Gly Tyr Ala Phe Asn Thr Ser Gly Asp Gly Glu Pro			
65	70	75	80
Ile Val Val Gly Phe His His Trp Gly Glu Ser Val Val Glu His Leu			
85	90	95	
Arg Gly Met Phe Gly Ile Ala Ile Trp Asp Thr Lys Glu Lys Ser Leu			
100	105	110	
Phe Leu Ala Arg Asp Gln Phe Gly Ile Lys Pro Leu Phe Tyr Ala Thr			
115	120	125	
Thr Glu His Gly Thr Val Phe Ser Ser Glu Lys Lys Thr Ile Leu Glu			
130	135	140	
Met Ala Glu Glu Met Asn Leu Asp Leu Gly Leu Asp Lys Arg Thr Ile			
145	150	155	160
Glu His Tyr Val Asp Leu Gln Tyr Val Pro Glu Pro Asp Thr Leu His			
165	170	175	
Ala Gln Ile Ser Arg Leu Glu Ser Gly Cys Thr Ala Thr Val Arg Pro			
180	185	190	
Gly Gly Lys Leu Glu Gln Lys Arg Tyr Phe Lys Pro Gln Phe Pro Val			
195	200	205	
Gln Lys Val Val Lys Gly Lys Glu Gln Asp Leu Phe Asp Arg Ile Ala			
210	215	220	
Gln Val Leu Glu Asp Ser Val Glu Lys His Met Arg Ala Asp Val Thr			
225	230	235	240
Val Gly Ser Phe Leu Phe Gly Gly Ile Asp Ser Thr Ala Ile Ala Ala			
245	250	255	
Leu Ala Lys Arg His Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe			
260	265	270	
Glu Arg Glu Gly Tyr Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala			
275	280	285	
Ala Ile Gly Ala Glu His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr			
290	295	300	
Ala Asn Ala Ile Pro Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala			
305	310	315	320
Asp Pro Ser Leu Val Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys			
325	330	335	

His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly  
 340 345 350  
 Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys  
 355 360 365  
 Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu  
 370 375 380  
 Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr  
 385 390 395 400  
 Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln  
 405 410 415  
 Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu  
 420 425 430  
 Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala  
 435 440 445  
 Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu  
 450 455 460  
 Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val  
 465 470 475 480  
 Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr  
 485 490 495  
 Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala  
 500 505 510  
 Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly  
 515 520 525  
 Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly  
 530 535 540  
 Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn  
 545 550 555 560  
 Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser  
 565 570 575  
 Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His  
 580 585 590  
 Gly Phe Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser  
 595 600 605  
 Tyr Pro Val Glu Leu  
 610

&lt;210&gt; 111

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXN00116

&lt;400&gt; 111

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tttgcgccacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115
                               Met Ser Asn Asp Phe
                               1           5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
                10                15                20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag gcc ttt 211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
                25                30                35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
                40                45                50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
                55                60                65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
                70                75                80                85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
                90                95                100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile
                105                110                115

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg 499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala
                120                125                130

ggg gcg acg cgg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg 547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp
                135                140                145

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg cgg 595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg
                150                155                160                165

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct 643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser
                170                175                180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg 691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu
                185                190                195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag 739

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Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln  
 200 205 210

aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg 787  
 Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val  
 215 220 225

acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg 835  
 Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr  
 230 235 240 245

ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg 883  
 Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala  
 250 255 260

aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg 931  
 Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val  
 265 270 275

gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag 979  
 Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys  
 280 285 290

ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg  
 1027  
 Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala  
 295 300 305

ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat  
 1075  
 Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp  
 310 315 320 325

att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag  
 1123  
 Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys  
 330 335 340

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag  
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 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys  
 345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg  
 1219  
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr  
 360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta  
 1261  
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 375 380 385

tagtttgaac aggttggttg ggg  
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<210> 112  
 <211> 387  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 112

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Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
 35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
 50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
 65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
 85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
 100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
 115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
 130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
 145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
 165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
 180 185 190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
 195 200 205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
 210 215 220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
 225 230 235 240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
 245 250 255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
 260 265 270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
 275 280 285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
 290 295 300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
 305 310 315 320

Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys  
355 360 365

Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile  
370 375 380

Lys Lys Leu  
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<210> 113

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 113

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Met Thr Gln Arg Ala  
1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163  
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp  
10 15 20

ggc cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211  
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly  
25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259  
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala  
40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307  
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp  
55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355  
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr  
70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403  
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro  
90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451  
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg  
105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499  
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val  
 120 125 130  
 gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547  
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val  
 135 140 145  
 aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
 150 155 160 165  
 aag cag ttg gcg 607  
 Lys Gln Leu Ala

<210> 114  
 <211> 169  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 114  
 Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
 1 5 10 15  
 Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
 20 25 30  
 Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
 35 40 45  
 Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
 50 55 60  
 Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
 65 70 75 80  
 Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val  
 85 90 95  
 Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu  
 100 105 110  
 Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser  
 115 120 125  
 Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr  
 130 135 140  
 Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe  
 145 150 155 160  
 Ser Lys Lys Ala Leu Lys Gln Leu Ala  
 165

<210> 115  
 <211> 1230  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1207)

&lt;223&gt; RXN00618

&lt;400&gt; 115

gctgcattag agggctgtat ctcgatctaa aagcagtagc cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgtc	atg cag atg ttg gac	115
	Met Gln Met Leu Asp	
	1 5	

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc	163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys	
10 15 20	

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca	211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala	
25 30 35	

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt	259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly	
40 45 50	

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat	307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr	
55 60 65	

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca	355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser	
70 75 80 85	

ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat	403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr	
90 95 100	

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa	451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu	
105 110 115	

tct ttg ggg gcg aag gct ctg aac ctg cgc tgc act gca gag act cgt	499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg	
120 125 130	

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag	547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys	
135 140 145	

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat	595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp	
150 155 160 165	

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct	643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala	
170 175 180	

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg	691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro	
185 190 195	

ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739  
 Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr  
           200                                  205                                  210

ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787  
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile  
           215                                  220                                  225

gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835  
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu  
           230                                  235                                  240                                  245

tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883  
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe  
                                   250                                  255                                  260

act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931  
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg  
                                   265                                  270                                  275

gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979  
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly  
                                   280                                  285                                  290

act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct  
 1027  
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser  
           295                                  300                                  305

gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa  
 1075  
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu  
           310                                  315                                  320                                  325

gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc  
 1123  
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly  
                                   330                                  335                                  340

cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att  
 1171  
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile  
                                   345                                  350                                  355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac  
 1217  
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
           360                                  365

taggttagtt tcg  
 1230

<210> 116

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp

1	5	10	15
Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala	20	25	30
Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr	35	40	45
Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp	50	55	60
His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val	65	70	75
Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu	85	90	95
Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr	100	105	110
Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys	115	120	125
Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu	130	135	140
Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr	145	150	155
Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys	165	170	175
Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met	180	185	190
Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala	195	200	205
Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg	210	215	220
Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn	225	230	235
Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala	245	250	255
Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His	260	265	270
Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro	275	280	285
Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu	290	295	300
Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu	305	310	315
Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe	325	330	335

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser  
 340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys  
 355 360 365

Lys

<210> 117

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA00618

<400> 117

cccaacgggc accatcattg atccggaaga gctagagcgc atcgccaagt ggtgcatga 60

caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115  
 Met Ser Phe Gly Arg  
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163  
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly  
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211  
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile  
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259  
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser  
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307  
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala  
 55 60 65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355  
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr  
 70 75 80 85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403  
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu  
 90 95 100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451  
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val  
 105 110 115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499  
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp  
 120 125 130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547

Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu  
 135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 118  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 118  
 Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 119  
 <211> 385  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA00627

&lt;400&gt; 119

gctgcattag agggtcgtat ctcgatctaa aagcagtagc cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115  
 Met Gln Met Leu Asp  
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
 70 75 80 85

ggg gga ttc gtg gca tcg ttt atc gcc acc 385  
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 90 95

&lt;210&gt; 120

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 120

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 85 90 95

<210> 121  
 <211> 1434  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1411)  
 <223> RXA02550

<400> 121  
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 tagctttcaa ctacgcacac aaagtggcaa cattgagcgg gtg act aca gac aag 115  
 Val Thr Thr Asp Lys  
 1 5  
 cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg 163  
 Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala  
 10 15 20  
 gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat 211  
 Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp  
 25 30 35  
 cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg 259  
 Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val  
 40 45 50  
 gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag 307  
 Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys  
 55 60 65  
 ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg 355  
 Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val  
 70 75 80 85  
 att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc 403  
 Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser  
 90 95 100  
 acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac 451  
 Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr  
 105 110 115  
 gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta 499  
 Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu  
 120 125 130  
 ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc 547  
 Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu  
 135 140 145  
 aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg 595  
 Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp  
 150 155 160 165  
 act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt 643  
 Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys

170	175	180	
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa			691
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys			
185	190	195	
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc			739
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro			
200	205	210	
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att			787
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile			
215	220	225	
gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc			835
Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg			
230	235	240	245
att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca			883
Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro			
250	255	260	
gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc			931
Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val			
265	270	275	
gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac			979
Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr			
280	285	290	
gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc			1027
Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu			
295	300	305	
tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga			1075
Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly			
310	315	320	325
cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa			1123
Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu			
330	335	340	
cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc			1171
Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser			
345	350	355	
tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc			1219
Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro			
360	365	370	
aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc			1267
Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu			
375	380	385	

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca  
1315

Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
1363

His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag  
1411

Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
425 430 435

tagtagttgt taggattcac cac  
1434

<210> 122

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn  
1 5 10 15

Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr  
20 25 30

Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu  
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly  
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe  
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr  
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala  
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val  
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr  
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro  
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro  
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu  
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile  
 195 200 205  
 Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu  
 210 215 220  
 Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp  
 225 230 235 240  
 Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu  
 245 250 255  
 Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser  
 260 265 270  
 Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
 275 280 285  
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
 290 295 300  
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
 305 310 315 320  
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
 325 330 335  
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
 340 345 350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
 355 360 365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
 370 375 380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
 385 390 395 400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
 405 410 415  
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
 420 425 430  
 Ser Thr Tyr Lys Gln  
 435

&lt;210&gt; 123

&lt;211&gt; 1701

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1678)

&lt;223&gt; RXA02193

&lt;400&gt; 123

cccccgaaaa tgtagtgggt agttccacac tgcctcttac aagtacgtag gataatccac 60

agcaccattg tgatttcctt caacttgtga gaggcagtag	atg tct aag acg agc	115
	Met Ser Lys Thr Ser	
	1 5	
aac aag tct tca gca gac tca aag aat gac gca aaa gcc gaa gac att		163
Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala Lys Ala Glu Asp Ile		
	10 15 20	
gtg aac ggc gag aac caa atc gcc acg aat gag tcg cag tct tca gac		211
Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu Ser Gln Ser Ser Asp		
	25 30 35	
agc gct gca gtt tcg gaa cgt gtc gtc gaa cca aaa acc acg gtt cag		259
Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro Lys Thr Thr Val Gln		
	40 45 50	
aaa aag ttc cga atc gaa tcg gat ctg ctt ggt gaa ctt cag atc cca		307
Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly Glu Leu Gln Ile Pro		
	55 60 65	
tcc cac gca tat tac ggg gtg cac acc ctt cgt gcg gtg gac aac ttc		355
Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Asp Asn Phe		
	70 75 80 85	
caa atc tca cga acc acc atc aac cac gtc cca gat ttc att cgc ggc		403
Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro Asp Phe Ile Arg Gly		
	90 95 100	
atg gtc cag gtg aaa aag gcc gca gct tta gca aac cgc cga ctg cac		451
Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala Asn Arg Arg Leu His		
	105 110 115	
aca ctt cca gca caa aaa gca gaa gca att gtc tgg gct tgt gat cag		499
Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val Trp Ala Cys Asp Gln		
	120 125 130	
atc ctc att gag gaa cgc tgt atg gat cag ttc ccc atc gat gtg ttc		547
Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe Pro Ile Asp Val Phe		
	135 140 145	
cag ggt ggc gca ggt acc tca ctg aac atg aac acc aac gag gtt gtt		595
<del>Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu Val Val</del>		
<del>150 155 160 165</del>		
gcc aac ctt gca ctt gag ttc tta ggc cat gaa aag ggc gag tac cac		643
Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu Lys Gly Glu Tyr His		
	170 175 180	
atc ctg cac ccc atg gat gat gtg aac atg tcc cag tcc acc aac gat		691
Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn Asp		
	185 190 195	
tcc tac cca act ggt ttc cgc ctg ggc att tac gct gga ctg cag acc		739
Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Gly Leu Gln Thr		
	200 205 210	
ctc atc gct gaa att gat gag ctt cag gtt gcg ttc cgc cac aag ggc		787
Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala Phe Arg His Lys Gly		
	215 220 225	

aat gag ttt gtc gac atc atc aag atg ggc cgc acc cag ttg cag gat 835  
 Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg Thr Gln Leu Gln Asp  
 230 235 240 245

gct gtt ccc atg agc ttg ggc gaa gag ttc cga gca ttc gcg cac aac 883  
 Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg Ala Phe Ala His Asn  
 250 255 260

ctc gca gaa gag cag acc gtg ctg cgt gaa gct gcc aac cgt ctc ctc 931  
 Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala Ala Asn Arg Leu Leu  
 265 270 275

gag gtc aat ctt ggt gca acc gca atc ggt act ggt gtg aac act cca 979  
 Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr Gly Val Asn Thr Pro  
 280 285 290

gca ggc tac cgc cac cag gtt gtc gct gct ctg tct gag gtc acc gga  
 1027  
 Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu Ser Glu Val Thr Gly  
 295 300 305

ctg gaa cta aag tcc gca cgt gat ctc atc gag gct acc tct gac acc  
 1075  
 Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu Ala Thr Ser Asp Thr  
 310 315 320 325

ggt gca tat gtt cat gcg cac tcc gca atc aag cgt gca gcc atg aaa  
 1123  
 Gly Ala Tyr Val His Ala His Ser Ala Ile Lys Arg Ala Ala Met Lys  
 330 335 340

ctg tcc aag atc tgt aac gat cta cgt ctg ctg tct tct ggt cct cgt  
 1171  
 Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg  
 345 350 355

gct ggc ttg aac gaa atc aac ctg cca cca cgc cag gct ggt tcc tcc  
 1219  
 Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg Gln Ala Gly Ser Ser  
 360 365 370

atc atg cca gcc aag gtc aac cca gtg atc cca gaa gtg gtc aac cag  
 1267  
 Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln  
 375 380 385

gtc tgc ttc aag gtc ttc ggt aac gat ctc acc gtc acc atg gct gcg  
 1315  
 Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr Met Ala Ala  
 390 395 400 405

gaa gct ggc cag ttg cag ctc aac gtc atg gag cca gtc att ggc gaa  
 1363  
 Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Glu  
 410 415 420

tcc ctc ttc cag tca ctg cgc atc ctg ggc aat gca gcc aag act ttg  
 1411  
 Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn Ala Ala Lys Thr Leu  
 425 430 435

cgt gag aag tgc gtc gta gga atc acc gcc aac gct gat gtt tgc cgt  
1459

Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg  
440 445 450

gct tac gtt gat aac tcc atc ggg att atc act tac ctg aac cca ttc  
1507

Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe  
455 460 465

ctg ggc cac gac att gga gat cag atc ggt aag gaa gca gcc gaa act  
1555

Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr  
470 475 480 485

ggc cga cca gtg cgt gaa ctc atc ctg gaa aag aag ctc atg gat gaa  
1603

Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu  
490 495 500

aag acg ctc gag gca gtc ctg tcc aag gag aac ctc atg cac cca atg  
1651

Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met  
505 510 515

ttc cgc gga agg ctc tac ttg gag aac taatccaaga tctcgtctga  
1698

Phe Arg Gly Arg Leu Tyr Leu Glu Asn  
520 525

tac  
1701

<210> 124

<211> 526

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Ser Lys Thr Ser Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala  
1 5 10 15

Lys Ala Glu Asp Ile Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu  
20 25 30

Ser Gln Ser Ser Asp Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro  
35 40 45

Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly  
50 55 60

Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg  
65 70 75 80

Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro  
85 90 95

Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala  
100 105 110

Asn Arg Arg Leu His Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val  
 115 120 125  
 Trp Ala Cys Asp Gln Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe  
 130 135 140  
 Pro Ile Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn  
 145 150 155 160  
 Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu  
 165 170 175  
 Lys Gly Glu Tyr His Ile Leu His Pro Met Asp Asp Val Asn Met Ser  
 180 185 190  
 Gln Ser Thr Asn Asp Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr  
 195 200 205  
 Ala Gly Leu Gln Thr Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala  
 210 215 220  
 Phe Arg His Lys Gly Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg  
 225 230 235 240  
 Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg  
 245 250 255  
 Ala Phe Ala His Asn Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala  
 260 265 270  
 Ala Asn Arg Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr  
 275 280 285  
 Gly Val Asn Thr Pro Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu  
 290 295 300  
 Ser Glu Val Thr Gly Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu  
 305 310 315 320  
 Ala Thr Ser Asp Thr Gly Ala Tyr Val His Ala His Ser Ala Ile Lys  
 325 330 335  
 Arg Ala Ala Met Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu  
 340 345 350  
 Ser Ser Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg  
 355 360 365  
 Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro  
 370 375 380  
 Glu Val Val Asn Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr  
 385 390 395 400  
 Val Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu  
 405 410 415  
 Pro Val Ile Gly Glu Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn  
 420 425 430  
 Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn

435	440	445	
Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr			
450	455	460	
Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys			
465	470	475	480
Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys			
	485	490	495
Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn			
	500	505	510
Leu Met His Pro Met Phe Arg Gly Arg Leu Tyr Leu Glu Asn			
	515	520	525

<210> 125  
 <211> 1098  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1075)  
 <223> RXA02432

<400> 125  
 cacgtgattc atttgtgacc aacaaccgaa actgagccag aagactgtca atccccctgct 60  
 gtgcacataa caactgcagc tagttgatac gctagagcgc atg tcg aag cag cac 115  
 Met Ser Lys Gln His  
 1 5  
 tcc aca cca tta aac aat gat gaa gaa cac act tcc gct cct caa aag 163  
 Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys  
 10 15 20  
 gtt gcg gta atc acc acg ggc gga acc atc gcc tgt act tcc gac gca 211  
 Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala  
 25 30 35

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aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259  
 Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro  
 40 45 50  
 atc gca cca cgg ttc aat gga gcg cag atc gct ttc gaa atc cac gaa 307  
 Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu  
 55 60 65  
 atc aac cgc ctt gat tcc tcc tcc atg acg ttt gag gat ctc gat tcc 355  
 Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser  
 70 75 80 85  
 atc atc gcc acg gtt cat aag gtg ttg gag gat ccg gat gtt gtt ggc 403  
 Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly  
 90 95 100  
 gta gta gtt acc cac ggc acc gat tcc atg gaa gag tcc gcc atc gcc 451  
 Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala

105	110	115	
gta gac acc ttc ctt gat gat ccc cgc cca gtc att ttc acc ggc gcc			499
Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val Ile Phe Thr Gly Ala			
120	125	130	
caa aaa ccc ttc gat cat ccc gaa gcc gac ggc cca aac aac ctt ttc			547
Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly Pro Asn Asn Leu Phe			
135	140	145	
gaa gcc tgc ctc atc gca tcc gac ccc tcc gct cgc gga att ggt gca			595
Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala Arg Gly Ile Gly Ala			
150	155	160	165
ctc att gtc ttc ggt cac gcc gtc atc cct gct cgc ggc tgc gtt aaa			643
Leu Ile Val Phe Gly His Ala Val Ile Pro Ala Arg Gly Cys Val Lys			
170	175	180	
tgg cac acc tct gat gag ctg gcg ttt gca acc aac ggc cct gaa gaa			691
Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr Asn Gly Pro Glu Glu			
185	190	195	
cca gag cgc ccc gat gcg ctg ccc gta gct aaa ttg gcg gat gtc tct			739
Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys Leu Ala Asp Val Ser			
200	205	210	
gtc gaa atc atc ccc gca tac cct ggt gcc acc ggc gca atg gtg gaa			787
Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr Gly Ala Met Val Glu			
215	220	225	
gct gcc atc gct gcc ggt gct caa gga ctt gta gtg gaa gca atg gga			835
Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val Val Glu Ala Met Gly			
230	235	240	245
tca ggc aat gtt ggt tcc cgc atg ggt gat gcc cta ggt aaa gca ctt			883
Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala Leu Gly Lys Ala Leu			
250	255	260	
gac gct gga att ccc gtg gtg atg agc act agg gtt cct cgt ggt gaa			931
Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg Val Pro Arg Gly Glu			
265	270	275	
gta tcc gga gtg tat ggc ggt gca ggt gga ggt gcg act ttg gct gcg			979
Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly Ala Thr Leu Ala Ala			
280	285	290	
aag ggc gct gtg gga tct cgc tac ttc aga gct ggt cag gca cgt att			
1027			
Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala Gly Gln Ala Arg Ile			
295	300	305	
ttg ctc gcg att gcc att gcg acg ggc gca cat ccg gtg acg ctt tac			
1075			
Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His Pro Val Thr Leu Tyr			
310	315	320	325
taatttcgcc cttggtcttg cat			
1098			

&lt;210&gt; 126

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 126

Met Ser Lys Gln His Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr  
 1 5 10 15

Ser Ala Pro Gln Lys Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala  
 20 25 30

Cys Thr Ser Asp Ala Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala  
 35 40 45

Asp Leu Leu Ala Pro Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala  
 50 55 60

Phe Glu Ile His Glu Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe  
 65 70 75 80

Glu Asp Leu Asp Ser Ile Ile Ala Thr Val His Lys Val Leu Glu Asp  
 85 90 95

Pro Asp Val Val Gly Val Val Val Thr His Gly Thr Asp Ser Met Glu  
 100 105 110

Glu Ser Ala Ile Ala Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val  
 115 120 125

Ile Phe Thr Gly Ala Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly  
 130 135 140

Pro Asn Asn Leu Phe Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala  
 145 150 155 160

Arg Gly Ile Gly Ala Leu Ile Val Phe Gly His Ala Val Ile Pro Ala  
 165 170 175

Arg Gly Cys Val Lys Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr  
 180 185 190

Asn Gly Pro Glu Glu Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys  
 195 200 205

Leu Ala Asp Val Ser Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr  
 210 215 220

Gly Ala Met Val Glu Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val  
 225 230 235 240

Val Glu Ala Met Gly Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala  
 245 250 255

Leu Gly Lys Ala Leu Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg  
 260 265 270

Val Pro Arg Gly Glu Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly  
 275 280 285

Ala Thr Leu Ala Ala Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala  
 290 295 300

Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His  
 305 310 315 320

Pro Val Thr Leu Tyr  
 325

<210> 127

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXN03003

<400> 127

tcgatgatct gggctcccca ggtggtgcgg ctaagcttgg accacaagat tttgatcacc 60

caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115  
 Met Thr Ser Arg Thr  
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163  
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser  
 10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211  
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser  
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259  
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu  
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307  
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro  
 55 60 65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag ccg cgc tac aac atg 355  
 Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met  
 70 75 80 85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403  
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu  
 90 95 100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451  
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val  
 105 110 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499  
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala  
 120 125 130

gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547  
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
 135 140 145

atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595  
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
 150 155 160 165

gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
 170 175 180

aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
 185 190 195

gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739  
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp  
 200 205 210

ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775  
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu  
 215 220 225

&lt;210&gt; 128

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 128

Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp  
 1 5 10 15

Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly  
 20 25 30

Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser  
 35 40 45

Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
 50 55 60

Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val  
 85 90 95

Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile  
 100 105 110

Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val  
 115 120 125

Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe  
 130 135 140

Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser  
 145 150 155 160

Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val  
 165 170 175

Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr

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180              185              190
Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp
    195              200              205

Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser
    210              215              220

Leu
225

<210> 129
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXN00508

<400> 129
agccacgtgt ttaaggatag ttgaaagcgt ggggcaatac tggcactaac cccggcacca 60

atcgtatttc tgcgcgcggt tgggtggcaca atagttcaac atg aac ttg ctg acc 115
                                         Met Asn Leu Leu Thr
                                         1           5

acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163
Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys
          10              15              20

caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211
Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala
          25              30              35

tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259
Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly
          40              45              50

gcg gat gcg ttt ggt gtg gca act ctt gcg gag gct atg cag ttg cgt 307
Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg
          55              60              65

gat atc ggc atc agc caa gag gtt ttg tgt tgg att tgg aca ccg gag 355
Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu
          70              75              80              85

cag gat ttc cgc gcc gcc att gat cgc aat att gat ttg gct gtt att 403
Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile
          90              95              100

tct ccc gcg cat gcc aaa gcc ttg atc gaa act gat gcg gag cat att 451
Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile
          105              110              115

cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcg ggt gtg gat 499
Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp
          120              125              130

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gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac 547  
 Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu Ala Ala Ala Pro His  
 135 140 145

att gag gtc acg ggc atg ttc acg cac ttg gcg tgc gcg gat gag cca 595  
 Ile Glu Val Thr Gly Met Phe Thr His Leu Ala Cys Ala Asp Glu Pro  
 150 155 160 165

gag aat ccg gaa act gat cgc caa att att gct ttt cga cgc gcc ctt 643  
 Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala Phe Arg Arg Ala Leu  
 170 175 180

gcg ctc gcc cgc aag cac ggg ctt gag tgc ccg gtc aac cac gta tgc 691  
 Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro Val Asn His Val Cys  
 185 190 195

aac tca cct gca ttc ttg act cga tct gat tta cac atg gag atg gtc 739  
 Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu His Met Glu Met Val  
 200 205 210

cga ccg ggt ttg gcc ttt tat ggg ttg gaa ccc gtg gcg gga ctg gag 787  
 Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro Val Ala Gly Leu Glu  
 215 220 225

cat ggt ttg aag ccg gcg atg acg tgg gag gcg aag gtg agc gtc gta 835  
 His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala Lys Val Ser Val Val  
 230 235 240 245

aag caa att gaa gct gga caa ggc act tcc tat ggc ctg acc tgg cgc 883  
 Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr Gly Leu Thr Trp Arg  
 250 255 260

gct gag gat cgc ggc ttt gtg gct gtg gtg cct gcg ggc tat gcc gat 931  
 Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro Ala Gly Tyr Ala Asp  
 265 270 275

ggc atg ccg cgg cat gcc cag ggg aaa ttc tcc gtc acg att gat ggc 979  
 Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser Val Thr Ile Asp Gly  
 280 285 290

ctg gac tat ccg cag gtt ggg cgc gta tgc atg gat cag ttc gtt att  
 1027

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Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met Asp Gln Phe Val Ile  
 295 300 305

tct ttg ggc gac aat cca cac ggc gtg gaa gct ggg gcg aag gcc gtg  
 1075

Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala Gly Ala Lys Ala Val  
 310 315 320 325

ata ttc ggt gag aat ggg cat gac gca act gat ttt gcg gag cgt tta  
 1123

Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp Phe Ala Glu Arg Leu  
 330 335 340

gac acc att aac tat gag gta gtg tgc cga cca acc ggc cga act gtc  
 1171

Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro Thr Gly Arg Thr Val  
 345 350 355

cgc gca tat gtt taagtgaata cgtttaagga gca

1206

Arg Ala Tyr Val

360

<210> 130

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

Met Asn Leu Leu Thr Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn  
1 5 10 15

Thr Arg Val Leu Lys Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val  
20 25 30

Val Lys Ala Asn Ala Tyr Asn His Gly Val Glu Lys Val Ala Pro Val  
35 40 45

Ile Ala Ala His Gly Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu  
50 55 60

Ala Met Gln Leu Arg Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp  
65 70 75 80

Ile Trp Thr Pro Glu Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile  
85 90 95

Asp Leu Ala Val Ile Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr  
100 105 110

Asp Ala Glu His Ile Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His  
115 120 125

Arg Ser Gly Val Asp Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu  
130 135 140

Ala Ala Ala Pro His Ile Glu Val Thr Gly Met Phe Thr His Leu Ala  
145 150 155 160

Cys Ala Asp Glu Pro Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala  
165 170 175

Phe Arg Arg Ala Leu Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro  
180 185 190

Val Asn His Val Cys Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu  
195 200 205

His Met Glu Met Val Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro  
210 215 220

Val Ala Gly Leu Glu His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala  
225 230 235 240

Lys Val Ser Val Val Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr  
245 250 255

Gly Leu Thr Trp Arg Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro

260	265	270
Ala Gly Tyr Ala Asp Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser		
275	280	285
Val Thr Ile Asp Gly Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met		
290	295	300
Asp Gln Phe Val Ile Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala		
305	310	315
Gly Ala Lys Ala Val Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp		
325	330	335
Phe Ala Glu Arg Leu Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro		
340	345	350
Thr Gly Arg Thr Val Arg Ala Tyr Val		
355	360	

<210> 131  
 <211> 1152  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1129)  
 <223> RXN00636

<400> 131  
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 tcgatctggc ccgttcgaac ataaggaata ttctactcc atg atg att gat aca 115  
 Met Met Ile Asp Thr  
 1 5  
 cct gct gtt ctc att gac cgc gag cgc tta act gcc aac att tcc agg 163  
 Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr Ala Asn Ile Ser Arg  
 10 15 20  
 atg gca gct cac gcc ggt gcc cat gag att gcc ctg cgt ccg cat gtg 211  
 Met Ala Ala His Ala Gly Ala His Glu Ile Ala Leu Arg Pro His Val  
 25 30 35  
 aaa acg cac aaa atc att gaa att gcg cag atg cag gtc gac gcc ggt 259  
 Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met Gln Val Asp Ala Gly  
 40 45 50  
 gcc cga ggg atc acc tgc gca acc att ggc gag gcg gaa att ttt gcc 307  
 Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu Ala Glu Ile Phe Ala  
 55 60 65  
 ggc gca ggt ttt acg gac atc ttt att gca tat ccg ctg tat cta acc 355  
 Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr Pro Leu Tyr Leu Thr  
 70 75 80 85  
 gat cat gca gtg caa cgc ctg aac gcg atc ccc gga gaa att tcc att 403  
 Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro Gly Glu Ile Ser Ile  
 90 95 100

ggc gtg gat tgc gta gag atg gca cag gcg acg gcg ggt ttg cgg gaa 451  
 Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr Ala Gly Leu Arg Glu  
 105 110 115

gat atc aag gct ctg att gaa gtg gat tgc gga cat cgt aga agt gga 499  
 Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly His Arg Arg Ser Gly  
 120 125 130

gtc acg gcg act gct tca gaa ttg agt cag atc cgc gag gcg ctg ggc 547  
 Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile Arg Glu Ala Leu Gly  
 135 140 145

agc agg tat gca gga gtg ttt act ttt cct ggg cat tct tat ggc cgg 595  
 Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly His Ser Tyr Gly Pro  
 150 155 160 165

gga aat ggt gag cag gca gca gct gat gag ctt cag gct cta aac aac 643  
 Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu Gln Ala Leu Asn Asn  
 170 175 180

agc gtc cag cga ctt gct ggc ggc ctg act tct ggc ggt tcc tgc cgg 691  
 Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser Gly Gly Ser Ser Pro  
 185 190 195

tct gcg cag ttt aca gac gca atc gat gag atg cga cca ggc gtg tat 739  
 Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met Arg Pro Gly Val Tyr  
 200 205 210

gtg ttt aac gat tcc cag cag atc acc tgc gga gca tgc act gag aag 787  
 Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly Ala Cys Thr Glu Lys  
 215 220 225

cag gtg gca atg acg gtg ctg tct act gtg gtc agc cga aat gtg tca 835  
 Gln Val Ala Met Thr Val Leu Ser Thr Val Val Ser Arg Asn Val Ser  
 230 235 240 245

gat cgt cgg atc att ttg gat gcg gga tcc aaa atc ctc agc act gat 883  
 Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys Ile Leu Ser Thr Asp  
 250 255 260

aaa cca gca tgg att gat ggc aat ggt ttt gtt ctg ggg aat cct gaa 931  
 Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val Leu Gly Asn Pro Glu  
 265 270 275

gcc cga atc tct gct ttg tgc gag cat cac gca acc att ttc tgg cca 979  
 Ala Arg Ile Ser Ala Leu Ser Glu His His Ala Thr Ile Phe Trp Pro  
 280 285 290

gat aaa gtg cta ctt cca gta atc ggg gag cag ctc aac atc gtg ccc  
 1027  
 Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln Leu Asn Ile Val Pro  
 295 300 305

aac cat gcc tgc aac gtg att aat ttg gtg gat gag gtc tac gtt cgg  
 1075  
 Asn His Ala Cys Asn Val Ile Asn Leu Val Asp Glu Val Tyr Val Arg  
 310 315 320 325

gaa gcc gat ggc act ttc cgt acc tgg aag gta gtt gcc cgc ggc aga  
 1123

Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val Val Ala Arg Gly Arg  
 330 335 340

aac aat tagggaaacc tcttgacctt cac  
 1152  
 Asn Asn

<210> 132  
 <211> 343  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 132  
 Met Met Ile Asp Thr Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr  
 1 5 10 15  
 Ala Asn Ile Ser Arg Met Ala Ala His Ala Gly Ala His Glu Ile Ala  
 20 25 30  
 Leu Arg Pro His Val Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met  
 35 40 45  
 Gln Val Asp Ala Gly Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu  
 50 55 60  
 Ala Glu Ile Phe Ala Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr  
 65 70 75 80  
 Pro Leu Tyr Leu Thr Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro  
 85 90 95  
 Gly Glu Ile Ser Ile Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr  
 100 105 110  
 Ala Gly Leu Arg Glu Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly  
 115 120 125  
 His Arg Arg Ser Gly Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile  
 130 135 140  
 Arg Glu Ala Leu Gly Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly  
 145 150 155 160  
 His Ser Tyr Gly Pro Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu  
 165 170 175  
 Gln Ala Leu Asn Asn Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser  
 180 185 190  
 Gly Gly Ser Ser Pro Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met  
 195 200 205  
 Arg Pro Gly Val Tyr Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly  
 210 215 220  
 Ala Cys Thr Glu Lys Gln Val Ala Met Thr Val Leu Ser Thr Val Val  
 225 230 235 240  
 Ser Arg Asn Val Ser Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys

[illegible]

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<210> 133
<211> 879
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(856)  
<223> RXA02536
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<400> 133  
aagaagtgat cacgcgaacc tgtgtataac ttgcctcaaa ggcctaggc tgtggattat 60

gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115  
Met Asp Asn Phe Ala  
1 5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163  
Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val  
10 15 20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211  
Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu  
25 30 35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259  
Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg  
40 45 50

aaa tta gcc gat gag ctg gac gtt qtc atc gtt gcg ggc atg ttc acc 307  
Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr  
55 60 65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355  
Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn  
70 75 80 85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403  
Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys  
90 95 100

att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451  
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys  
                   105                  110                  115

ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499  
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly  
                   120                  125                  130

gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547  
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu  
                   135                  140                  145

gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595  
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp  
                   150                  155                  160                  165

ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643  
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala  
                   170                  175                  180

ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691  
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro  
                   185                  190                  195

gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739  
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser  
                   200                  205                  210

atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787  
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu  
                   215                  220                  225

cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835  
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile  
                   230                  235                  240                  245

cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879  
 Arg Glu Ala Leu Pro Val Leu  
                   250

&lt;210&gt; 134

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 134

Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu  
   1                  5                  10                  15

Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe  
                   20                  25                  30

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe  
                   35                  40                  45

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val  
                   50                  55                  60

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr

65	70	75	80
Ile Ser Arg Val Asn Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His	85	90	95
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu	100	105	110
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp	115	120	125
Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu	130	135	140
Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro	145	150	155
Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu	165	170	175
Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly	180	185	190
Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr	195	200	205
Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala	210	215	220
Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser	225	230	235
Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu	245	250	

&lt;210&gt; 135

&lt;211&gt; 1635

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1612)

&lt;223&gt; RXS00870

&lt;400&gt; 135

caagacggcg atgtcgccgc cgctgttgat accgcagcgc gacttggttca cacagatatt 60

caacaattca cttcgagag catttaagga atttacacac atg tct gaa cca caa	115
Met Ser Glu Pro Gln	
1 5	

acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc	163
Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly	
10 15 20	

aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat	211
Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn	
25 30 35	

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc	259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala	
40 45 50	
acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa	307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln	
55 60 65	
gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag	355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu	
70 75 80 85	
ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc	403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala	
90 95 100	
atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt	451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly	
105 110 115	
ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc	499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly	
120 125 130	
att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc	547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile	
135 140 145	
agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc	595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile	
150 155 160 165	
gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat	643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979

Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile  
 280 285 290  
 gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac  
 1027  
 Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp  
 295 300 305  
 acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac  
 1075  
 Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His  
 310 315 320 325  
 ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat  
 1123  
 Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr  
 330 335 340  
 gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt  
 1171  
 Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg  
 345 350 355  
 aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg  
 1219  
 Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr  
 360 365 370  
 ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc  
 1267  
 Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile  
 375 380 385  
 ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca  
 1315  
 Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala  
 390 395 400 405  
 att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc  
 1363  
 Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe  
 410 415 420  
 acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg  
 1411  
 Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val  
 425 430 435  
 ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac  
 1459  
 Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His  
 440 445 450  
 tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat  
 1507  
 Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr  
 455 460 465  
 ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc  
 1555  
 Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser

470                      475                      480                      485

cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca  
1603

Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro  
                    490                      495                      500

cag aac gat taattgaagg agagcacagg act  
1635

Gln Asn Asp

<210> 136  
<211> 504  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 136

Met Ser Glu Pro Gln Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser  
1                      5                      10                      15

Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly  
                    20                      25                      30

Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala  
                    35                      40                      45

Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser  
50                      55                      60

Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn  
65                      70                      75                      80

Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys  
                    85                      90                      95

Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val  
                    100                      105                      110

Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu  
115                      120                      125

Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly  
130                      135                      140

Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met  
145                      150                      155                      160

Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys  
                    165                      170                      175

Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp  
                    180                      185                      190

Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp  
195                      200                      205

Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile  
210                      215                      220

Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser  
 225 230 235 240  
 Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His  
 245 250 255  
 Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala  
 260 265 270  
 Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser  
 275 280 285  
 Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile  
 290 295 300  
 Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu  
 305 310 315 320  
 Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp  
 325 330 335  
 Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile  
 340 345 350  
 Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe  
 355 360 365  
 Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala  
 370 375 380  
 Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala  
 385 390 395 400  
 Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn  
 405 410 415  
 Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln  
 420 425 430  
 His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val  
 435 440 445  
 Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly  
 450 455 460  
 Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu  
 465 470 475 480  
 Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile  
 485 490 495  
 Asn Leu Gly Phe Pro Gln Asn Asp  
 500

&lt;210&gt; 137

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(508)

&lt;223&gt; RXS02299

&lt;400&gt; 137

acgcgggggt tgttgccgga tcgaaatatt cctttccttg tcattctcacg ctatgatttc 60

taaaacttgc	aggacaaccc	ccataaggac	accacaggac	atg	ctg	cgc	acc	atc	115
				Met	Leu	Arg	Thr	Ile	
				1				5	

ctc	gga	agt	aag	att	cac	cga	gcc	act	gtc	act	caa	gct	gat	cta	gat	163
Leu	Gly	Ser	Lys	Ile	His	Arg	Ala	Thr	Val	Thr	Gln	Ala	Asp	Leu	Asp	
				10					15					20		

tat	gtt	ggc	tct	gta	acc	atc	gac	gcc	gac	ctg	gtt	cac	gcc	gcc	gga	211
Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu	Val	His	Ala	Ala	Gly	
			25					30					35			

ttg	atc	gaa	ggc	gaa	aaa	gtt	gcc	atc	gta	gac	atc	acc	aac	ggc	gct	259
Leu	Ile	Glu	Gly	Glu	Lys	Val	Ala	Ile	Val	Asp	Ile	Thr	Asn	Gly	Ala	
		40					45					50				

cgt	ctg	gaa	act	tat	gtc	att	gtg	ggc	gac	gcc	gga	acg	ggc	aat	att	307
Arg	Leu	Glu	Thr	Tyr	Val	Ile	Val	Gly	Asp	Ala	Gly	Thr	Gly	Asn	Ile	
	55					60					65					

tgc	atc	aat	ggt	gcc	gct	gca	cac	ctt	att	aat	cct	ggc	gat	ctt	gtg	355
Cys	Ile	Asn	Gly	Ala	Ala	Ala	His	Leu	Ile	Asn	Pro	Gly	Asp	Leu	Val	
	70				75					80				85		

atc	atc	atg	agc	tac	ctt	cag	gca	act	gat	gcg	gaa	gcc	aag	gcg	tat	403
Ile	Ile	Met	Ser	Tyr	Leu	Gln	Ala	Thr	Asp	Ala	Glu	Ala	Lys	Ala	Tyr	
				90					95					100		

gag	cca	aag	att	gtg	cac	gtg	gac	gcc	gac	aac	cgc	atc	gtt	gcg	ctc	451
Glu	Pro	Lys	Ile	Val	His	Val	Asp	Ala	Asp	Asn	Arg	Ile	Val	Ala	Leu	
		105					110						115			

ggc	aac	gat	ctt	gcg	gaa	gca	cta	cct	gga	tcc	ggg	ctt	ttg	acg	tcg	499
Gly	Asn	Asp	Leu	Ala	Glu	Ala	Leu	Pro	Gly	Ser	Gly	Leu	Leu	Thr	Ser	
		120					125					130				

aga	agc	att	tagcgtttta	gctcgccaat	att	531
Arg	Ser	Ile				
		135				

&lt;210&gt; 138

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 138

Met	Leu	Arg	Thr	Ile	Leu	Gly	Ser	Lys	Ile	His	Arg	Ala	Thr	Val	Thr
1				5					10					15	

Gln	Ala	Asp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu
		20					25						30		

Val	His	Ala	Ala	Gly	Leu	Ile	Glu	Gly	Glu	Lys	Val	Ala	Ile	Val	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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          35              40              45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
   50              55              60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
   65              70              75              80
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
          85              90              95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
          100              105              110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
          115              120              125
Gly Leu Leu Thr Ser Arg Ser Ile
          130              135

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<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1030)
<223> RXA01561

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taataatggt cattttcatc gagttctaga aaacacaggc atg ctc acc ctc aac 115
                                     Met Leu Thr Leu Asn
                                     1              5
gat gtc atc acc gcc caa caa cga acc gcc cct cat gtt cga cga acg 163
Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro His Val Arg Arg Thr
          10              15              20
cca ctt ttc gaa gca gac ccc atc gac ggc aca caa atc tgg atc aaa 211
Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr Gln Ile Trp Ile Lys
          25              30              35
gca gag ttc ctc caa aag tgc ggc gtg ttc aaa acg cgt gga gca ttc 259
Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys Thr Arg Gly Ala Phe
          40              45              50
aac cgc cag ctc gca gct tcg gaa aac qga cta ctc gac cca acg gtt 307
Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu Leu Asp Pro Thr Val
          55              60              65
ggc atc gtc gcg gca tca ggc gga aac gca gga ctc gca aat gct ttt 355
Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly Leu Ala Asn Ala Phe
          70              75              80              85
gcc gca gca tcc tta agc gtt ccc gcc acg gta ttg gtg ccc gaa act 403
Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val Leu Val Pro Glu Thr
          90              95              100

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gcc cca caa gta aaa gtt gat cgc ctc aag caa tac ggt gca acc gtg 451
Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln Tyr Gly Ala Thr Val
105 110 115

caa caa atc gga tct gaa tat gcg gaa gca ttt gag gca gct caa acc 499
Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe Glu Ala Ala Gln Thr
120 125 130

ttt gag tcg gaa act ggt gct ctg ttt tgc cac gcc tac gac cag ccc 547
Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His Ala Tyr Asp Gln Pro
135 140 145

gac atc gca gct gga gca ggc gtc att ggg cta gaa att gtc gaa gat 595
Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu Glu Ile Val Glu Asp
150 155 160 165

ctt ccc gac gtt gac acc atc gtg gtt gct gtc ggt ggc ggt gga ctc 643
Leu Pro Asp Val Asp Thr Ile Val Val Ala Val Gly Gly Gly Gly Leu
170 175 180

tat gca gga atc gca gcc gtc gta gca gcc cac gac atc aaa gtg gtg 691
Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His Asp Ile Lys Val Val
185 190 195

gcc gtt gaa ccc tcc aaa att cca acc ctg cac aac tca ctc att gcc 739
Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His Asn Ser Leu Ile Ala
200 205 210

ggc caa cca gtc gat gtg aac gtt tct ggt atc gcg gca gat tct ttg 787
Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile Ala Ala Asp Ser Leu
215 220 225

ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat 835
Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His
230 235 240 245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga 883
Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg
250 255 260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc 931
Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala
265 270 275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat 979
Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp
280 285 290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca
1027
Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr
295 300 305

ctg tgatgtgatt tcaaacgata aca
1053
Leu
310

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&lt;210&gt; 140

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 140

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Met Leu Thr Leu Asn Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro
  1             5             10             15

His Val Arg Arg Thr Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr
      20             25             30

Gln Ile Trp Ile Lys Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys
      35             40             45

Thr Arg Gly Ala Phe Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu
      50             55             60

Leu Asp Pro Thr Val Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly
      65             70             75             80

Leu Ala Asn Ala Phe Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val
      85             90             95

Leu Val Pro Glu Thr Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln
      100            105            110

Tyr Gly Ala Thr Val Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe
      115            120            125

Glu Ala Ala Gln Thr Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His
      130            135            140

Ala Tyr Asp Gln Pro Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu
      145            150            155            160

Glu Ile Val Glu Asp Leu Pro Asp Val Asp Thr Ile Val Val Ala Val
      165            170            175

Gly Gly Gly Gly Leu Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His
      180            185            190

Asp Ile Lys Val Val Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His
      195            200            205

Asn Ser Leu Ile Ala Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile
      210            215            220

Ala Ala Asp Ser Leu Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp
      225            230            235            240

Ile Ala Thr Ala His Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala
      245            250            255

Ile Ile Ala Ala Arg Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala
      260            265            270

Glu His Gly Ala Ala Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr
      275            280            285

Lys Pro Ala Ala Asp Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn
      290            295            300

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Thr Asp Leu Thr Thr Leu  
305 310

<210> 141  
<211> 1470  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1447)  
<223> RXA01850

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tcaccttgta caccaccaga gaaaaggccc accctcagcc atg gct atc agt gtt 115  
Met Ala Ile Ser Val  
1 5  
ggt gat cta ttt agc atc ggt atc gga cca tca tcc tca cat acc gtc 163  
Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser Ser Ser His Thr Val  
10 15 20  
ggc ccc atg aga gcc gcc ctc acg tat atc tct gaa ttt ccc agc tcg 211  
Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser Glu Phe Pro Ser Ser  
25 30 35  
cat gtc gat atc acg ttg cac gga tcc ctt gcc gcc acc ggt aaa ggc 259  
His Val Asp Ile Thr Leu His Gly Ser Leu Ala Ala Thr Gly Lys Gly  
40 45 50  
cac tgc act gac cgg gcg gta tta ctg ggt ctg gtg gga tgg gaa cca 307  
His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu Val Gly Trp Glu Pro  
55 60 65  
acg ata gtt ccc att gat gct gca ccc tca ccc ggc gcg ccg att cct 355  
Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro Gly Ala Pro Ile Pro  
70 75 80 85  
gcg aaa ggt cct gtg aac ggg cca aag gga acg gtg tcg tat tcc ctg 403  
Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr Val Ser Tyr Ser Leu  
90 95 100  
acg ttt gat cct cat cct ctt cca gaa cac ccc aat gcc gtt acc ttt 451  
Thr Phe Asp Pro His Pro Leu Pro Glu His Pro Asn Ala Val Thr Phe  
105 110 115  
aaa gga tca acc aca agg act tat ttg tcg gtg ggt ggt ggg ttc att 499  
Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val Gly Gly Gly Phe Ile  
120 125 130  
atg acg ttg gag gat ttc cgg aag ctg gac gat atc gga tca ggt gtg 547  
Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp Ile Gly Ser Gly Val  
135 140 145  
tca acc att cat cca gag gca gag gtg cct tgt cct ttt cag aag agt 595  
Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys Pro Phe Gln Lys Ser  
150 155 160 165

tcc caa tta ctc gca tat ggt cgc gat ttt gcg gag gtc atg aag gat 643  
 Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala Glu Val Met Lys Asp  
 170 175 180

aat gag cgc tta atc cac ggg gat ctt ggc aca gtg gat gcc cat ttg 691  
 Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr Val Asp Ala His Leu  
 185 190 195

gat cga gtg tgg cag att atg cag gag tgc gtg gca caa ggc atc gca 739  
 Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val Ala Gln Gly Ile Ala  
 200 205 210

acg ccg ggg att tta ccg ggt ggg ttg aat gtg caa cgt cgg gcg ccg 787  
 Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val Gln Arg Arg Ala Pro  
 215 220 225

cag gta cac gcg ctg att agc aac ggg gat acg tgt gag ctg ggt gct 835  
 Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr Cys Glu Leu Gly Ala  
 230 235 240 245

gat ctt gat gct gtg gag tgg gtg aat ctg tac gcc ttg gcg gtg aat 883  
 Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr Ala Leu Ala Val Asn  
 250 255 260

gaa gaa aac gcc gct ggt ggt cgt gtg gtt act gct ccg act aat ggt 931  
 Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly  
 265 270 275

gct gcg ggg att att ccg gcg gtg atg cac tat gcg ccg gat ttt ttg 979  
 Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr Ala Arg Asp Phe Leu  
 280 285 290

aca ggt ttt ggg gcg gag cag gcg ccg acg ttt ttg tat acc gcg ggt  
 1027  
 Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe Leu Tyr Thr Ala Gly  
 295 300 305

gcg gtg ggc atc atc att aag gaa aat gcc tcg atc tct ggc gcg gag  
 1075  
 Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser Ile Ser Gly Ala Glu  
 310 315 320 325

gtg ggg tgt cag ggt gag gtt ggt tca gcg tcc gcg atg gcg gct gcc  
 1123  
 Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser Ala Met Ala Ala Ala  
 330 335 340

ggg ttg tgt gca gtc tta ggt ggt tct ccg caa cag gtg gaa aac gcc  
 1171  
 Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln Gln Val Glu Asn Ala  
 345 350 355

gcg gag att gcg ttg gag cac aat ttg gga ttg acg tgc gat ccg gtg  
 1219  
 Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu Thr Cys Asp Pro Val  
 360 365 370

ggc ggg tta gtg cag att ccg tgt att gaa cgc aac gct att gct gcc  
 1267  
 Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala Ile Ala Ala

375                      380                      385  
 atg aag tcc atc aat gcg gca agg ctt gcc cgg att ggt gat ggc aac  
 1315  
 Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg Ile Gly Asp Gly Asn  
 390                      395                      400                      405  
 aat cgc gtg agt ttg gat gat gtg gtg gtc acg atg gct gcc acc ggc  
 1363  
 Asn Arg Val Ser Leu Asp Asp Val Val Val Thr Met Ala Ala Thr Gly  
 410                      415                      420  
 cgg gac atg ctg acc aaa tat aag gaa acg tcc ctt ggt ggt ttg gca  
 1411  
 Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu Ala  
 425                      430                      435  
 acc acc ttg ggc ttc ccg gtg tcg atg acg gag tgt tagcgggtacg  
 1457  
 Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu Cys  
 440                      445  
 gctttaacac ggc  
 1470

<210> 142  
 <211> 449  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 142  
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 1                      5                      10                      15  
 Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser  
 20                      25                      30  
 Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala  
 35                      40                      45  
 Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu  
 50                      55                      60  
 Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro  
 65                      70                      75                      80  
 Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr  
 85                      90                      95  
 Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro  
 100                      105                      110  
 Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val  
 115                      120                      125  
 Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp  
 130                      135                      140  
 Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys  
 145                      150                      155                      160

Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala  
 165 170 175  
 Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr  
 180 185 190  
 Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val  
 195 200 205  
 Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val  
 210 215 220  
 Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr  
 225 230 235 240  
 Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr  
 245 250 255  
 Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr  
 260 265 270  
 Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr  
 275 280 285  
 Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe  
 290 295 300  
 Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser  
 305 310 315 320  
 Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser  
 325 330 335  
 Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln  
 340 345 350  
 Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu  
 355 360 365  
 Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg  
 370 375 380  
 Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg  
 385 390 395 400  
 Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr  
 405 410 415  
 Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser  
 420 425 430  
 Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu  
 435 440 445  
 Cys

&lt;210&gt; 143

&lt;211&gt; 1425

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1402)

&lt;223&gt; RXA00580

&lt;400&gt; 143

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ttacgcgcgg gattcgtctt gtgaaagggt agctgacctg atg acc gat gcc cac	115
Met Thr Asp Ala His	
1 5	

caa gcg gac gat gtc cgt tac cag cca ctg aac gag ctt gat cct gag	163
Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn Glu Leu Asp Pro Glu	
10 15 20	

gtg gct gct gcc atc gct ggg gaa ctt gcc cgt caa cgc gat aca tta	211
Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg Gln Arg Asp Thr Leu	
25 30 35	

gag atg atc gcg tct gag aac ttc gtt ccc cgt tct gtt ttg cag gcg	259
Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ser Val Leu Gln Ala	
40 45 50	

cag ggt tct gtt ctt acc aat aag tat gcc gag ggt tac cct ggc cgc	307
Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Gly Arg	
55 60 65	

cgt tac tac ggt ggt tgc gaa caa gtt gac atc att gag gat ctt gca	355
Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile Ile Glu Asp Leu Ala	
70 75 80 85	

cgt gat cgt gcg aag gct ctc ttc ggt gca gag ttc gcc aat gtt cag	403
Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala Asn Val Gln	
90 95 100	

cct cac tct ggc gca cag gct aat gct gct gtg ctg atg act ttg gct	451
Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu Met Thr Leu Ala	
105 110 115	

gag cca ggc gac aag atc atg ggt ctg tct ttg gct cat ggt ggt cac	499
Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His Gly Gly His	
120 125 130	

ttg acc cac gga atg aag ttg aac ttc tcc gga aag ctg tac gag gtt	547
Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu Tyr Glu Val	
135 140 145	

gtt gcg tac ggt gtt gat cct gag acc atg cgt gtt gat atg gat cag	595
Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg Val Asp Met Asp Gln	
150 155 160 165	

gtt cgt gag att gct ctg aag gag cag cca aag gta att atc gct ggc	643
Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys Val Ile Ile Ala Gly	
170 175 180	

tgg tct gca tac cct cgc cac ctt gat ttc gag gct ttc cag tct att	691
Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu Ala Phe Gln Ser Ile	

185	190	195	
gct gcg gaa gtt ggc gcg aag ctg tgg gtc gat atg gct cac ttc gct			739
Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp Met Ala His Phe Ala			
200	205	210	
ggt ctt gtt gct gct ggt ttg cac cca agc cca gtt cct tac tct gat			787
Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro Val Pro Tyr Ser Asp			
215	220	225	
ggt gtt tct tcc act gtc cac aag act ttg ggt gga cct cgt tcc ggc			835
Val Val Ser Ser Thr Val His Lys Thr Leu Gly Gly Pro Arg Ser Gly			
230	235	240	245
atc att ctg gct aag cag gag tac gcg aag aag ctg aac tct tcc gta			883
Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys Leu Asn Ser Ser Val			
250	255	260	
ttc cca ggt cag cag ggt ggt cct ttg atg cac gca gtt gct gcg aag			931
Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His Ala Val Ala Ala Lys			
265	270	275	
gct act tct ttg aag att gct ggc act gag cag ttc cgt gac cgt cag			979
Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln Phe Arg Asp Arg Gln			
280	285	290	
gct cgc acg ttg gag ggt gct cgc att ctt gct gag cgt ctg act gct			
1027			
Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala Glu Arg Leu Thr Ala			
295	300	305	
tct gat gcg aag gcc gct ggc gtg gat gtc ttg acc ggt ggc act gat			
1075			
Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu Thr Gly Gly Thr Asp			
310	315	320	325
gtg cac ttg gtt ttg gct gat ctg cgt aac tcc cag atg gat ggc cag			
1123			
Val His Leu Val Leu Ala Asp Leu Arg Asn Ser Gln Met Asp Gly Gln			
330	335	340	
cag gcg gaa gat ctg ctg cac gag gtt ggt atc act gtg aac cgt aac			
1171			
Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile Thr Val Asn Arg Asn			
345	350	355	
gcg gtt cct ttc gat cct cgt cca cca atg gtt act tct ggt ctg cgt			
1219			
Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val Thr Ser Gly Leu Arg			
360	365	370	
att ggt act cct gcg ctg gct acc cgt ggt ttc gat att cct gca ttc			
1267			
Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe Asp Ile Pro Ala Phe			
375	380	385	
act gag gtt gca gac atc att ggt act gct ttg gct aat ggt aag tcc			
1315			
Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu Ala Asn Gly Lys Ser			
390	395	400	405

gca gac att gag tct ctg cgt ggc cgt gta gca aag ctt gct gca gat  
1363

Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp  
410 415 420

tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc  
1412

Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr Ile Val  
425 430

tttgagtttt cat  
1425

<210> 144

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Thr Asp Ala His Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn  
1 5 10 15

Glu Leu Asp Pro Glu Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg  
20 25 30

Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg  
35 40 45

Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu  
50 55 60

Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile  
65 70 75 80

Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu  
85 90 95

Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val  
100 105 110

Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu  
115 120 125

Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly  
130 135 140

Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg  
145 150 155 160

Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys  
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Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu  
180 185 190

Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp  
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Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro  
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Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly  
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Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys  
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Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala  
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Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile  
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Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe  
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Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu  
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 Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu

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Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu			
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Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly			
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Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu			
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Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg			
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&lt;210&gt; 146

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 146

Arg Asn Ser Gln Gly Lys Trp Cys Pro Ser Thr Arg Ser Pro Lys Asn
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Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu
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Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
35 40 45

Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
50 55 60

Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu
65 70 75 80

Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly
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Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg
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&lt;210&gt; 147

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Trp His Leu Ser Asn Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln
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 Met Thr Asp Phe Pro  
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 Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly  
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Tyr	Asn	Thr	Pro	Ala	Val	Ala	Thr	Leu	Met	Leu	Asp	Asn	Gln	Val			
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 Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu  
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 Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser  
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Gly His Leu Ser Phe Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser  
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&lt;210&gt; 153

&lt;211&gt; 1422

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1399)

&lt;223&gt; RXN02758

&lt;400&gt; 153

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Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu			
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Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu			
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Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro			
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1171			
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1267			
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His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu			
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<212> PRT

<213> Corynebacterium glutamicum

<400> 154

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Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg  
35 40 45

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Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu  
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Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His  
85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg  
100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala  
115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn  
130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu  
145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met  
165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala  
180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe  
195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala  
210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala  
225 230 235 240

Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys  
 245 250 255

Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala  
 260 265 270

Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg  
 275 280 285

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu  
 290 295 300

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr  
 305 310 315 320

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile  
 325 330 335

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp  
 340 345 350

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn  
 355 360 365

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala  
 370 375 380

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe  
 385 390 395 400

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp  
 405 410 415

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn  
 420 425 430

Ala

&lt;210&gt; 155

&lt;211&gt; 490

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(490)

&lt;223&gt; FRXA02479

&lt;400&gt; 155

atacatctca cccaattccc cataactaga caattgccca gcaacgactg ataagtctcc 60

aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc 115  
 Val Thr Glu Leu Ile  
 1 5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163  
 Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val  
 10 15 20

```

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
      25                      30                      35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
      40                      45                      50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
      55                      60                      65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
      70                      75                      80                      85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
      90                      95                      100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
      105                      110                      115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ctg gat 490
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp
      120                      125                      130

```

&lt;210&gt; 156

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 156

```

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
  1                      5                      10                      15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
      20                      25                      30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
      35                      40                      45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
      50                      55                      60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
      65                      70                      75                      80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
      85                      90                      95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
      100                      105                      110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
      115                      120                      125

Leu Asp
      130

```

<210> 157  
 <211> 558  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(535)  
 <223> FRXA02758

<400> 157  
 aaggcggttg ctgggtttgga tgcgtcggtg atcgatgagg tgcgtgccgc tattgagctg 60  
 acccttggtg cgcgcaccac gatccgtacg gttgaaccgc atg ggt tac cag acc 115  
 Met Gly Tyr Gln Thr  
 1 5  
 gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag 163  
 Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu  
 10 15 20  
 gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat 211  
 Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp  
 25 30 35  
 ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 259  
 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala  
 40 45 50  
 aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 307  
 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met  
 55 60 65  
 tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 355  
 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu  
 70 75 80 85  
 tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 403  
 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys  
 90 95 100  
 gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 451  
 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu  
 105 110 115  
 cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 499  
 His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu  
 120 125 130  
 gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 545  
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala  
 135 140 145  
 tttctcgacg ccc 558

<210> 158  
 <211> 145  
 <212> PRT

<213> Corynebacterium glutamicum

<400> 158

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Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
 1             5             10             15

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
      20             25             30

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
      35             40             45

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
      50             55             60

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
      65             70             75             80

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
      85             90             95

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
      100            105            110

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
      115            120            125

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
      130            135            140

Ala
145

```

<210> 159

<211> 205

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (72)..(182)

<223> FRXA02759

<400> 159

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tcttacttct aagctgaatg tgatattgcg attaagcggt ctgggttgct gcgctggtct 60

aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110
      Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val
      1             5             10

att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158
Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala
      15             20             25

gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205
Val Thr Glu Arg Ala Met Arg Gly
      30             35

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<210> 160

gaa	gcc	gca	gca	acc	caa	gcc	gtc	gca	gcg	atc	tac	ggc	atg	gag	ctc	307
Glu	Ala	Ala	Ala	Thr	Gln	Ala	Val	Ala	Ala	Ile	Tyr	Gly	Met	Glu	Leu	
	55					60					65					
aac	gaa	ttc	aac	gca	ggt	gtc	gac	gcc	gtc	gcc	ggc	gcc	atc	gaa	tct	355
Asn	Glu	Phe	Asn	Ala	Gly	Val	Asp	Ala	Val	Ala	Gly	Ala	Ile	Glu	Ser	
	70				75					80					85	
gcc	ggc	gcc	atc	cac	gtc	agc	atc	ccc	gat	ccc	gat	gtc	ccc	caa	gat	403
Ala	Gly	Ala	Ile	His	Val	Ser	Ile	Pro	Asp	Pro	Asp	Val	Pro	Gln	Asp	
				90					95					100		
gtc	gga	gcc	gca	gca	ttt	ttc	gac	gtc	gac	aac	acc	ctc	atc	caa	ggc	451
Val	Gly	Ala	Ala	Ala	Phe	Phe	Asp	Val	Asp	Asn	Thr	Leu	Ile	Gln	Gly	
			105					110				115				
tcc	tcc	ctc	atc	gtt	ttc	gcc	caa	gga	ctc	ttc	cgg	aag	aaa	ttc	ttc	499

Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe Arg Lys Lys Phe Phe  
 120 125 130  
 acc atc aaa gaa atc ctc ccc gtg gtg tgg aaa caa gtg aaa ttc aaa 547  
 Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys Gln Val Lys Phe Lys  
 135 140 145  
 ctc acc ggc tcc gaa aac gcc gac gac gtc tcc cgc ggc cgc gaa caa 595  
 Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser Arg Gly Arg Glu Gln  
 150 155 160 165  
 gcc ctc gaa ttc atc aaa ggc cgc ccc gtc caa gaa cta gtt gac ctc 643  
 Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln Glu Leu Val Asp Leu  
 170 175 180  
 tgc gaa gaa atc gtc gac caa cgc atg gcc gac aaa atg tgg ccc ggc 691  
 Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp Lys Met Trp Pro Gly  
 185 190 195  
 acc aaa caa ctc gcc gac atg cac atc gcc gcc ggc cac caa gtc tgg 739  
 Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala Gly His Gln Val Trp  
 200 205 210  
 ctc gtc tcc gca acc ccc gtc caa ctc gcc caa atc ctg gca caa cgc 787  
 Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln Ile Leu Ala Gln Arg  
 215 220 225  
 ctc ggc ttc acc gga gcg atc ggc aca gtc gca gaa gca aaa gat gga 835  
 Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala Glu Ala Lys Asp Gly  
 230 235 240 245  
 gta ttc acc ggc cga ctc gtc ggc gac atc ctc cac gga ccc ggc aaa 883  
 Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu His Gly Pro Gly Lys  
 250 255 260  
 aga cac gca gtc gca gca ctc gca tcc atc gaa caa ctc gac ctc acc 931  
 Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu Gln Leu Asp Leu Thr  
 265 270 275  
 cga tgc acc gcc tac tcc gac tcc atc aac gac ctc ccc atg ctc tcc 979  
 Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp Leu Pro Met Leu Ser  
 280 285 290  
 atg gtc ggc acc gcc gtc gca gta aac ccc gac tcc aaa ctc cgc aaa  
 1027  
 Met Val Gly Thr Ala Val Ala Val Asn Pro Asp Ser Lys Leu Arg Lys  
 295 300 305  
 gaa gcc gaa acc cga ggc tgg gac gtc cgc gat ttc cga agc atc cgc  
 1075  
 Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp Phe Arg Ser Ile Arg  
 310 315 320 325  
 aaa gcc acc cgc gaa tac gga atc ccc gcc ctg gtc acc gcc gca ttc  
 1123  
 Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu Val Thr Ala Ala Phe  
 330 335 340  
 agt gtc gcc ggc tgg agt cta cgc cgc cga tgg aga aaa caa  
 1165  
 Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp Arg Lys Gln

345

350

355

taacgcacag gagccgtttt aag  
1188

&lt;210&gt; 162

&lt;211&gt; 355

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 162

Met Ser Ser Glu Gly Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly  
1 5 10 15

Thr Pro Glu Asp Phe Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu  
20 25 30

Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala  
35 40 45

Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile  
50 55 60

Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala  
65 70 75 80

Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro  
85 90 95

Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn  
100 105 110

Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe  
115 120 125

Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys  
130 135 140

Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser  
145 150 155 160

Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln  
165 170 175

Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp  
180 185 190

Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala  
195 200 205

Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln  
210 215 220

Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala  
225 230 235 240

Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu  
245 250 255

His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu

<400> 163															
ggttgggggc atcaaaggat gcggacatcg ctgtgggggt gtgtaataat tgcacctgtg															60
aggtgccttt ctggcagggtg aatcaggact ctaagcaagc ttg att ctt cca gtt															115
Leu Ile Leu Pro Val															
1 5															
cag gag ggc att tcc tat ttt ccc acg cgg tta cac ctg aat cac atc															163
Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile															
10 15 20															
ggt gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc															211
Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu															
25 30 35															
gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc															259
Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe															
40 45 50															
ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc															307
Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr															
55 60 65															
tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att															355
Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile															
70 75 80 85															
gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat															403
Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr															
90 95 100															

ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac 451  
 Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr  
                   105                                  110                                  115

agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc 499  
 Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys  
                   120                                  125                                  130

acg tat aga aag cta acc ttt tta agt gcg cgg ttt taggggtgaga 545  
 Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe  
                   135                                  140                                  145

atctaacgct gag 558

<210> 164  
 <211> 145  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 164  
 Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu  
   1                                  5                                  10                                  15

His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp  
                   20                                  25                                  30

Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys  
                   35                                  40                                  45

Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser  
                   50                                  55                                  60

Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala  
                   65                                  70                                  75                                  80

Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys  
                                   85                                  90                                  95

Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn  
                   100                                  105                                  110

Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro  
                   115                                  120                                  125

Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg  
                   130                                  135                                  140

Phe  
 145

<210> 165  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (62)..(664)

&lt;223&gt; RXS01130

&lt;400&gt; 165

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agttcgtggc ggatgctgtg aacgtttccg gtggctcgct gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1           5           10           15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
      20           25           30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
      35           40           45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
      50           55           60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
      65           70           75           80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
      85           90           95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
      100           105           110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
      115           120           125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
      130           135           140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
      145           150           155           160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
      165           170           175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
      180           185           190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
      195           200

tga 687

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&lt;210&gt; 166

<211> 201  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 166

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Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
  1           5           10           15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
          20           25           30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
          35           40           45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
          50           55           60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
          65           70           75           80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
          85           90           95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
          100          105          110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
          115          120          125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
          130          135          140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
          145          150          155          160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
          165          170          175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
          180          185          190

Ala Thr Ser Phe Gln Val Asp Leu Asp
          195          200
  
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<210> 167  
 <211> 604  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(604)  
 <223> RXS03112

<400> 167

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gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtgag ggcgagtgga agcgggtcttc tttcaacggt gtg gaa att ttc gga 115
                               Val Glu Ile Phe Gly
                               1           5
  
```

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163  
 Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala  
                   10                  15                  20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211  
 Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr  
                   25                  30                  35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259  
 Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu  
                   40                  45                  50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307  
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys  
                   55                  60                  65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355  
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser  
                   70                  75                  80                  85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403  
 Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp  
                   90                  95                  100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451  
 Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala  
                   105                  110                  115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499  
 Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe  
                   120                  125                  130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547  
 Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu  
                   135                  140                  145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595  
 Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys  
                   150                  155                  160                  165

gcg ctg gct 604  
 Ala Leu Ala

&lt;210&gt; 168

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 168

Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Glu Phe Gly His Ile  
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Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val  
                   20                  25                  30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val  
                   35                  40                  45

Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr  
50 55 60

Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His  
65 70 75 80

Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg  
85 90 95

Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly  
100 105 110

His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr  
115 120 125

Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu  
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Asp Ser Val Leu Lys Ala Leu Ala  
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<211> 1458

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<213> Corynebacterium glutamicum

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<222> (101)..(1435)

<223> RXN00969

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Met Thr Ser Ala Ser  
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gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163  
Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile  
10 15 20

gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211  
Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met  
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acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259  
Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu  
40 45 50

gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307  
Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val  
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gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355  
Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu  
70 75 80 85

gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403  
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg  
90 95 100

gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451  
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala  
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Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp Ala Ala  
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gaa gcc gca aac gtt gac ctg tac ttc gag gct gct gtt gca tgc gca 547  
Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala Ala Val Ala Cys Ala  
135 140 145

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Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu Ala Gly Asp Gln Ile  
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Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr Asn Phe Ile Leu Asp  
170 175 180

gcc atg gat tcc acc ggc gct gac tat gca gat tct ttg gct gag gca 691  
Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp Ser Leu Ala Glu Ala  
185 190 195

act cgt ttg ggt tac gcc gaa gct gat cca act gca aac gtc gaa ggc 739  
Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr Ala Asn Val Glu Gly  
200 205 210

cat gac gcc gca tcc aag gct gca att ttg gca tgc atc gct ttc cac 787  
His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala Cys Ile Ala Phe His  
215 220 225

acc cgt gtt acc gcg gat gat gtg tac tgc gaa ggt att agg aac atc 835  
Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu Gly Ile Arg Asn Ile  
230 235 240 245

aac gct gcc gac att gag gca gca cag cag gca ggc cac acc atc aag 883  
Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala Gly His Thr Ile Lys  
250 255 260

ttg ttg gcc atc tgt gag aag ttc acc aac aag gaa gga aag tcg gct 931  
Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys Glu Gly Lys Ser Ala  
265 270 275

att tct gct cgc gtg cac ccg act cta tta cct gtg tcc cac cca ctg 979  
Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro Val Ser His Pro Leu  
280 285 290

gcg tcg gta aac aag tcc ttt aat gca atc ttt gtt gaa gca gaa gca 1027  
Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe Val Glu Ala Glu Ala  
295 300 305

gct ggt cgc ctg atg ttc tac gga aac ggt gca ggt ggc gcg cca acc 1075  
Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala Gly Gly Ala Pro Thr

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1123
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cac ggt ggc cgt gct cca ggt gag tcc acc tac gct aac ctg ccg atc
1171
His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr Ala Asn Leu Pro Ile
          345          350          355

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1219
Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His Leu Asp Met Asp Val
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1267
Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala Ser Leu Phe Ser Glu
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1315
Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu Glu Arg Asp Asp Asp
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gca cgt ctg atc gtg gtc acc cac tct gcg ctg gaa tct gat ctt tcc
1363
Ala Arg Leu Ile Val Val Thr His Ser Ala Leu Glu Ser Asp Leu Ser
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cgc acc gtt gaa ctg ctg aag gct aag cct gtt gtt aag gca atc aac
1411
Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val Val Lys Ala Ile Asn
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Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
          50          55          60

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Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala  
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 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly  
 85 90 95  
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys  
 100 105 110  
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu  
 115 120 125  
 Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala  
 130 135 140  
 Ala Val Ala Cys Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu  
 145 150 155 160  
 Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr  
 165 170 175  
 Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp  
 180 185 190  
 Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr  
 195 200 205  
 Ala Asn Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala  
 210 215 220  
 Cys Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu  
 225 230 235 240  
 Gly Ile Arg Asn Ile Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala  
 245 250 255  
 Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys  
 260 265 270  
 Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro  
 275 280 285  
 Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe  
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 Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala  
 305 310 315 320  
 Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala  
 325 330 335  
 Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr  
 340 345 350  
 Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His  
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 Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala  
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Met Thr Ser Ala Ser																
1 5																
gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att																163
Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile																
10 15 20																
gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg																211
Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met																
25 30 35																
acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag																259
Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu																
40 45 50																
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gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt																403
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg																
90 95 100																
gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc																451
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala																
105 110 115																
aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat																493
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp																
120 125 130																



Thr	Val	Glu	Val	Glu	Ile	Ile	Pro	Ser	Gly	Leu	Glu	Val	Glu	Val	Phe	
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Gly	Glu	Gly	Gln	Gly	Glu	Val	Pro	Leu	Asp	Gly	Ser	His	Leu	Val	Val	
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aaa	gct	att	cgt	gct	ggc	ctg	aag	gca	gct	gac	gct	gaa	gtt	cct	gga	355
Lys	Ala	Ile	Arg	Ala	Gly	Leu	Lys	Ala	Ala	Asp	Ala	Glu	Val	Pro	Gly	
	70				75					80					85	
ttg	cga	gtg	gtg	tgc	cac	aac	aac	att	ccg	cag	tct	cgt	ggt	ctt	ggc	403
Leu	Arg	Val	Val	Cys	His	Asn	Asn	Ile	Pro	Gln	Ser	Arg	Gly	Leu	Gly	
				90					95					100		
tcc	tct	gct	gca	gcg	gcg	gtt	gct	ggg	gtt	gct	gca	gct	aat	ggg	ttg	451
Ser	Ser	Ala	Ala	Ala	Ala	Val	Ala	Gly	Val	Ala	Ala	Ala	Asn	Gly	Leu	
			105					110					115			
gcg	gat	ttc	ccg	ctg	act	caa	gag	cag	att	gtt	cag	ttg	tcc	tct	gcc	499
Ala	Asp	Phe	Pro	Leu	Thr	Gln	Glu	Gln	Ile	Val	Gln	Leu	Ser	Ser	Ala	
		120					125					130				
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Phe	Glu	Gly	His	Pro	Asp	Asn	Ala	Ala	Ala	Ser	Val	Leu	Gly	Gly	Ala	
	135					140					145					
gtg	gtg	tcg	tgg	aca	aat	ctg	tct	atc	gac	ggc	aag	agc	cag	cca	cag	595
Val	Val	Ser	Trp	Thr	Asn	Leu	Ser	Ile	Asp	Gly	Lys	Ser	Gln	Pro	Gln	
	150				155					160					165	
tat	gct	gct	gta	cca	ctt	gag	gtg	cag	gac	aat	att	cgt	gcg	act	gcg	643
Tyr	Ala	Ala	Val	Pro	Leu	Glu	Val	Gln	Asp	Asn	Ile	Arg	Ala	Thr	Ala	
				170					175					180		
ctg	gtt	cct	aat	ttc	cac	gca	tcc	acc	gaa	gct	gtg	cgc	cga	gtc	ctt	691
Leu	Val	Pro	Asn	Phe	His	Ala	Ser	Thr	Glu	Ala	Val	Arg	Arg	Val	Leu	
			185					190					195			
ccc	act	gaa	gtc	act	cac	atc	gat	gcg	cga	ttt	aac	gtg	tcc	cgc	gtt	739
Pro	Thr	Glu	Val	Thr	His	Ile	Asp	Ala	Arg	Phe	Asn	Val	Ser	Arg	Val	
		200					205					210				
gca	gtg	atg	atc	gtt	gcg	ttg	cag	cag	cgt	cct	gat	ttg	ctg	tgg	gag	787
Ala	Val	Met	Ile	Val	Ala	Leu	Gln	Gln	Arg	Pro	Asp	Leu	Leu	Trp	Glu	
	215					220					225					
ggg	act	cgt	gac	cgt	ctg	cac	cag	cct	tat	cgt	gca	gaa	gtg	ttg	cct	835
Gly	Thr	Arg	Asp	Arg	Leu	His	Gln	Pro	Tyr	Arg	Ala	Glu	Val	Leu	Pro	
	230				235					240					245	
att	acc	tct	gag	tgg	gta	aac	cgc	ctg	cgc	aac	cgt	ggc	tac	gcg	gca	883
Ile	Thr	Ser	Glu	Trp	Val	Asn	Arg	Leu	Arg	Asn	Arg	Gly	Tyr	Ala	Ala	
				250					255					260		
tac	ctt	tcc	ggg	gcc	ggc	cca	acc	gcc	atg	gtg	ctg	tcc	act	gag	cca	931
Tyr	Leu	Ser	Gly	Ala	Gly	Pro	Thr	Ala	Met	Val	Leu	Ser	Thr	Glu	Pro	
			265					270						275		
att	cca	gac	aag	gtt	ttg	gaa	gat	gct	cgt	gag	tct	ggc	att	aag	gtg	979
Ile	Pro	Asp	Lys	Val	Leu	Glu	Asp	Ala	Arg	Glu	Ser	Gly	Ile	Lys	Val	

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                     20                      25                      30  
  
 Leu Ser Val Tyr Asp Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu  
                     35                      40                      45  
  
 Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly  
                     50                      55                      60  
  
 Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp  
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 Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln  
                     85                      90                      95  
  
 Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Ala Val Ala Gly Val Ala  
                     100                      105                      110  
  
 Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val  
                     115                      120                      125  
  
 Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser  
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 Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly  
                     145                      150                      155                      160  
  
 Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn  
                     165                      170                      175  
  
 Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala  
                     180                      185                      190  
  
 Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe  
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 Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro  
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 Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg  
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Ala Glu Val Leu Pro Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn  
245 250 255

Arg Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val  
260 265 270

Leu Ser Thr Glu Pro Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu  
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Glu Val Asn Gln Pro  
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<223> RXA00330

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Val Asp Tyr Ile Ser  
1 5

acg cgt gat gcc agc cgt acc cct gcc cgc ttc agt gat att ttg ctg 163  
Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe Ser Asp Ile Leu Leu  
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ggc ggt cta gca cca gac ggc gga ctg tac ctg cct gca acc tac cct 211  
Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu Pro Ala Thr Tyr Pro  
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caa cta gat gat gcc cag ctg agt aaa tgg cgt gag gta tta gcc aac 259  
Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg Glu Val Leu Ala Asn  
40 45 50

gaa gga tac gca gct ttg gct gct gaa gtt atc tcc ctg ttt gtt gat 307  
Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile Ser Leu Phe Val Asp  
55 60 65

gac atc cca gta gaa gac atc aag gcg atc acc gca cgc gcc tac acc 355  
Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr Ala Arg Ala Tyr Thr  
70 75 80 85

tac ccg aag ttc aac agc gaa gac atc gtt cct gtc acc gaa ctc gag 403  
Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro Val Thr Glu Leu Glu  
90 95 100

gac aac att tac ctg ggc cac ctt tcc gaa ggc cca acc gct gca ttc 451  
Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly Pro Thr Ala Ala Phe  
105 110 115

aaa gac atg gcc atg cag ctg ctc ggc gaa ctt ttc gaa tac gag ctt 499  
 Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu Phe Glu Tyr Glu Leu  
 120 125 130

cgc cgc cgc aac gaa acc atc aac atc ctg ggc gct acc tct ggc gat 547  
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acc ggc tcc tct gcg gaa tac gcc atg cgc ggc cgc gag gga atc cgc 595  
 Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly Arg Glu Gly Ile Arg  
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gta ttc atg ctg acc cca gct ggc cgc atg acc cca ttc cag caa gca 643  
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 170 175 180

cag atg ttt ggc ctt gac gat cca aac atc ttc aac atc gcc ctc gac 691  
 Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe Asn Ile Ala Leu Asp  
 185 190 195

ggc gtt ttc gac gat tgc caa gac gta gtc aag gct gtc tcc gcc gac 739  
 Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys Ala Val Ser Ala Asp  
 200 205 210

gca gaa ttc aaa aaa gac aac cgc atc ggt gcc gtg aac tcc atc aac 787  
 Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala Val Asn Ser Ile Asn  
 215 220 225

tgg gca cgc ctt atg gca cag gtt gtg tac tac gtt tcc tca tgg atc 835  
 Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr Val Ser Ser Trp Ile  
 230 235 240 245

cgc acc aca acc agc aat gac caa aag gtc agc ttc tcc gta cca acc 883  
 Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser Phe Ser Val Pro Thr  
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ggc aac ttc ggt gac att tgc gca ggc cac atc gcc cgc caa atg gga 931  
 Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile Ala Arg Gln Met Gly  
 265 270 275

ctt ccc atc gat cgc ctc atc gtg gcc acc aac gaa aac gat gtg ctc 979  
 Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn Glu Asn Asp Val Leu  
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 295 300 305

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 Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg Asp Ala Thr Arg Val  
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Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly Gly Phe Ser Leu Ala  
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Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu Tyr Gly Phe Ala Ser  
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gga cga tcc acc cat gct gac cgt gtg gca acc atc gct gac gtg cat  
1267

Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr Ile Ala Asp Val His  
375 380 385

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1315

Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr Ala Asp Gly Val His  
390 395 400 405

gtg gca cgc cag tgg agg gac gag gtc aac acc cca atc atc gtc cta  
1363

Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr Pro Ile Ile Val Leu  
410 415 420

gaa act gca ctc cca gtg aaa ttt gcc gac acc atc gtc gaa gca att  
1411

Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr Ile Val Glu Ala Ile  
425 430 435

ggt gaa gca cct caa act cca gag cgt ttc gcc gcg atc atg gat gct  
1459

Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala Ala Ile Met Asp Ala  
440 445 450

cca ttc aag gtt tcc gac cta cca aac gac acc gat gca gtt aag cag  
1507

Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr Asp Ala Val Lys Gln  
455 460 465

tac ata gtc gat gcg att gca aac act tcc gtg aag taacttgctt  
1553

tyr ile val asp ala ile ala asn thr ser val lys  
470 475 480

tacgcccaagg cct  
1566

<210> 176

<211> 481

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Val Asp Tyr Ile Ser Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe  
1 5 10 15

Ser Asp Ile Leu Leu Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu  
20 25 30

Pro Ala Thr Tyr Pro Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg  
           35                          40                          45  
 Glu Val Leu Ala Asn Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile  
           50                          55                          60  
 Ser Leu Phe Val Asp Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr  
           65                          70                          75                          80  
 Ala Arg Ala Tyr Thr Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro  
                                   85                          90                          95  
 Val Thr Glu Leu Glu Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly  
                           100                          105                          110  
 Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu  
           115                          120                          125  
 Phe Glu Tyr Glu Leu Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly  
           130                          135                          140  
 Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly  
           145                          150                          155                          160  
 Arg Glu Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr  
                           165                          170                          175  
 Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe  
                           180                          185                          190  
 Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys  
           195                          200                          205  
 Ala Val Ser Ala Asp Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala  
           210                          215                          220  
 Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr  
           225                          230                          235                          240  
 Val Ser Ser Trp Ile Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser  
                           245                          250                          255  
 Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile  
                           260                          265                          270  
 Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn  
           275                          280                          285  
 Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val  
           290                          295                          300  
 Arg Ser Ser Ala Asp Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile  
           305                          310                          315                          320  
 Ser Arg Ala Ser Asn Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg  
                           325                          330                          335  
 Asp Ala Thr Arg Val Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly  
           340                          345                          350  
 Gly Phe Ser Leu Ala Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu

355					360					365					
Tyr	Gly	Phe	Ala	Ser	Gly	Arg	Ser	Thr	His	Ala	Asp	Arg	Val	Ala	Thr
	370					375					380				
Ile	Ala	Asp	Val	His	Ser	Arg	Leu	Asp	Val	Leu	Ile	Asp	Pro	His	Thr
385					390					395					400
Ala	Asp	Gly	Val	His	Val	Ala	Arg	Gln	Trp	Arg	Asp	Glu	Val	Asn	Thr
				405					410					415	
Pro	Ile	Ile	Val	Leu	Glu	Thr	Ala	Leu	Pro	Val	Lys	Phe	Ala	Asp	Thr
			420					425					430		
Ile	Val	Glu	Ala	Ile	Gly	Glu	Ala	Pro	Gln	Thr	Pro	Glu	Arg	Phe	Ala
		435					440					445			
Ala	Ile	Met	Asp	Ala	Pro	Phe	Lys	Val	Ser	Asp	Leu	Pro	Asn	Asp	Thr
	450					455					460				
Asp	Ala	Val	Lys	Gln	Tyr	Ile	Val	Asp	Ala	Ile	Ala	Asn	Thr	Ser	Val
465					470					475					480
Lys															

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<210> 177
<211> 1254
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1231)
<223> RXN00403
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<400> 177
tttttcagac tcgtgagaat gcaaaactaga ctagacagag ctgtccatat acactggacg 60
aagtttttagt cttgtccacc cagaacaggc ggttattttc atg ccc acc ctc gcg    115
                                     Met Pro Thr Leu Ala
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cct	tca	ggt	caa	ctt	gaa	atc	caa	gcg	atc	ggt	gat	gtc	tcc	acc	gaa	163
Pro	Ser	Gly	Gln	Leu	Glu	Ile	Gln	Ala	Ile	Gly	Asp	Val	Ser	Thr	Glu	
				10					15					20		
gcc	gga	gca	atc	att	aca	aac	gct	gaa	atc	gcc	tat	cac	cgc	tgg	ggc	211
Ala	Gly	Ala	Ile	Ile	Thr	Asn	Ala	Glu	Ile	Ala	Tyr	His	Arg	Trp	Gly	
			25					30					35			
gaa	tac	cgc	gta	gat	aaa	gaa	gga	cgc	agc	aat	gtc	gtt	ctc	atc	gaa	259
Glu	Tyr	Arg	Val	Asp	Lys	Glu	Gly	Arg	Ser	Asn	Val	Val	Leu	Ile	Glu	
		40					45					50				
cac	gcc	ctc	act	gga	gat	tcc	aac	gca	gcc	gat	tgg	tgg	gct	gac	ttg	307
His	Ala	Leu	Thr	Gly	Asp	Ser	Asn	Ala	Ala	Asp	Trp	Trp	Ala	Asp	Leu	
	55					60					65					
ctc	ggt	ccc	ggc	aaa	gcc	atc	aac	act	gat	att	tac	tgc	gtg	atc	tgt	355

Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys  
 70 75 80 85  
 acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403  
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met  
 90 95 100  
 cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451  
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile  
 105 110 115  
 cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499  
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile  
 120 125 130  
 acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547  
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr  
 135 140 145  
 cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595  
 Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val  
 150 155 160 165  
 ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643  
 Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser  
 170 175 180  
 gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691  
 Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn  
 185 190 195  
 tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739  
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg  
 200 205 210  
 cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787  
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg  
 215 220 225  
 ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835  
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg  
 230 235 240 245  
 aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883  
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260  
 gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275  
 gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290  
 aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
1075

Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
1123

Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
1171

Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc  
1219

Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile  
360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag  
1254

Glu Phe Tyr Ile  
375

<210> 178

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
145 150 155 160

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile  
370 375

1

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa	163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu	
10 15 20	
gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Val	
150 155 160 165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883

Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg  
 1210  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser  
 360 365 370

<210> 180

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
355 360 365

Pro Ser  
370

<210> 181

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)..(748)

&lt;223&gt; RXC01207

&lt;400&gt; 181

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atTTTTgaac aatccccaca ccaacttcag gagaaaaaca gtg agc aga atc tat 115
                               Val Ser Arg Ile Tyr
                               1 5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
                               10 15 20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
                               25 30 35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
                               40 45 50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
                               55 60 65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
                               70 75 80 85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
                               90 95 100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
                               105 110 115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
                               120 125 130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
                               135 140 145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat 595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
                               150 155 160 165

gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                               170 175 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
                               185 190 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu

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200 205 210 771  
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 Ser Leu Arg  
 215

<210> 182  
 <211> 216  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 182  
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 Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu  
 20 25 30  
 Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu  
 35 40 45  
 Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro  
 50 55 60  
 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His  
 65 70 75 80  
 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly  
 85 90 95  
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu  
 100 105 110  
 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val  
 115 120 125  
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala  
 130 135 140  
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln  
 145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala  
 165 170 175  
 Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys  
 180 185 190  
 Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu  
 195 200 205  
 Gly Val Ser Ala Glu Ser Leu Arg  
 210 215

<210> 183  
 <211> 1419  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

&lt;223&gt; RXC00152

&lt;400&gt; 183

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caaatagtagc tggccattcc caactaaaac tggagtaacg atg aca gga cta atc 115
                                         Met Thr Gly Leu Ile
                                         1 5

ctc gcc ata gtt ttc ctg gtc ttt gtc gcc gtc gtg gtg atc aag tcc 163
Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser
              10              15              20

ata gcc ctg att ccc cag ggt gaa gcc gcc gtc att gaa cgc ctt ggt 211
Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly
              25              30              35

agc tac acc cgc acc gtt tca ggt ggc ctg acc ctg ctg gtt cca ttc 259
Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe
              40              45              50

gtg gac cga gta cgc gca agg atc gac acc cgt gag cgc gtg gtc tca 307
Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser
              55              60              65

ttc cca ccg cag gct gtt att acc caa gac aac ctg acc gtg gcc atc 355
Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile
              70              75              80              85

gat atc gtg gtg acc ttc caa atc aac gaa cca gag cgc gcc atc tac 403
Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro Glu Arg Ala Ile Tyr
              90              95              100

ggc gtg gac aac tac atc gtc ggt gtg gag cag att tct gta gca aca 451
Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln Ile Ser Val Ala Thr
              105              110              115

ctt cga gac gtt gtc ggt ggc atg acc ctg gaa gaa acc ctc act tca 499
Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu Glu Thr Leu Thr Ser
              120              125              130

cgt gac gtg atc aac cgc cgc ctc cgt ggc gag ctc gat gca gca acc 547
Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr
              135              140              145

acc aaa tgg ggc ctg cgc atc agc cgt gtg gaa cta aag gca att gat 595
Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu Leu Lys Ala Ile Asp
              150              155              160              165

ccg cca cca tcc atc cag caa tcg atg gaa aag cag atg aag gca gac 643
Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys Gln Met Lys Ala Asp
              170              175              180

cgt gaa aag cgc gcc acc att ttg acc gca gaa ggt cag cgc gaa gcc 691
Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu Gly Gln Arg Glu Ala
              185              190              195

gac atc aaa act gcc gaa ggt gaa aag caa gcc aag atc ctc caa gct 739

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Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala Lys Ile Leu Gln Ala  
 200 205 210

gag ggt gaa aag cac gca tcc atc ctg aac gca gaa gca gaa cgc caa 787  
 Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala Glu Ala Glu Arg Gln  
 215 220 225

gcg atg atc ctg cgc gcc gaa ggt gaa cgc gca gca cgc tac ctc cag 835  
 Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala Ala Arg Tyr Leu Gln  
 230 235 240 245

gcg cag ggt gaa gcc cga gca atc caa aag gtc aac gca gca atc aag 883  
 Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val Asn Ala Ala Ile Lys  
 250 255 260

tct gcc aag ttg acc cca gag gtt ctt gct tat caa tac ctc gaa aag 931  
 Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr Gln Tyr Leu Glu Lys  
 265 270 275

ctt cct aag atc gca gag ggc aac gcc tcc aag atg tgg gtc atc cca 979  
 Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys Met Trp Val Ile Pro  
 280 285 290

agc cag ttc tcc gat tct ctg gaa ggt ttt gcg aag cag ttc ggc gca  
 1027  
 Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala Lys Gln Phe Gly Ala  
 295 300 305

aag gat gca gaa ggt gtc ttc cgc tac gaa cca aac acc gtg gat gaa  
 1075  
 Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro Asn Thr Val Asp Glu  
 310 315 320 325

gaa acc cgc gac atc gca aac gcc gac aac gtg gaa gac tgg ttc tcc  
 1123  
 Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val Glu Asp Trp Phe Ser  
 330 335 340

acc gaa tca gac cct gaa atc gca gca gca gtc gcc gca gca aac gcc  
 1171  
 Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val Ala Ala Ala Asn Ala  
 345 350 355

gtg gcc aac aag cca gtc gat cca gaa ccc ggt gag atc ctt tcc aag  
 1219  
 Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly Glu Ile Leu Ser Lys  
 360 365 370

aag acc gca cga cgc gtt gaa cct gaa gca gta ttg gag gct ttg caa  
 1267  
 Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val Leu Glu Ala Leu Gln  
 375 380 385

aac gga acc act aca caa cct gag gtt gag gca gca cct cct acc gca  
 1315  
 Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala Ala Pro Pro Thr Ala  
 390 395 400 405

aac ttc gcc caa gaa ttc cct gca cca cag gca aac cct gaa gat tac  
 1363  
 Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala Asn Pro Glu Asp Tyr

269

Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val  
 245 250 255

Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr  
 260 265 270

Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys  
 275 280 285

Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala  
 290 295 300

Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro  
 305 310 315 320

Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val  
 325 330 335

Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val  
 340 345 350

Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly  
 355 360 365

Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val  
 370 375 380

Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala  
 385 390 395 400

Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala  
 405 410 415

Asn Pro Glu Asp Tyr Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn  
 420 425 430

&lt;210&gt; 185

&lt;211&gt; 1170

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1147)

&lt;223&gt; RXA00115

&lt;400&gt; 185

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cgtatattgt gacctacacc ccatactgtt aggagttttc atg ctc gac aat agt 115  
 Met Leu Asp Asn Ser  
 1 5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163  
 Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly  
 10 15 20

cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct	211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala	
25 30 35	
tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc	259
Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu	
40 45 50	
att ccg acg tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac	307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr	
55 60 65	
atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc	355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser	
70 75 80 85	
atc aac caa atc ggt aat ggt ttg tgc gtc tcc cct gcc aac acg gct	403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala	
90 95 100	
gat gac agc atc tgc atg tcc aag ttc ccg aat gtt cgc att ggt gat	451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp	
105 110 115	
gat gtc gtt gcc cag gac ccg ctc ttg cgc caa gag ttt ggt att acc	499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr	
120 125 130	
gag ctc ttt gcc gtc gtt ggt ggt tgc atg ggt gcg cag caa acc tat	547
Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr	
135 140 145	
gag tgg att gtt cgc ttc cct gac caa gtt cat cga gca gct ccg atc	595
Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile	
150 155 160 165	
gcg ggc act gcg aag aac act cct cat gat ttc atc ttc acc cag act	643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr	
170 175 180	
ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac	691
Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Glu Tyr	
185 190 195	
tcc tcc cat gaa gag gta gct gat gga ctt cgc cgt caa tgc cat ctt	739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu	
200 205 210	
tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg	787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp	
215 220 225	
cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc gcg gac ttc ctg	835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu	
230 235 240 245	
gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct	883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala	
250 255 260	

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931  
 Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu  
 265 270 275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979  
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile  
 280 285 290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca  
 1027  
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala  
 295 300 305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac  
 1075  
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His  
 310 315 320 325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa  
 1123  
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys  
 330 335 340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct  
 1170  
 Asn Leu Lys Glu Leu Phe Glu Ser  
 345

<210> 186

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu  
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Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Gly Gly Val Ile Glu  
 20 25 30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys  
 35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr  
 50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys  
 65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser  
 85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn  
 100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln  
 115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly  
 130 135 140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His  
145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe  
165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe  
180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg  
195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp  
210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val  
225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr  
245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His  
260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr  
275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys  
290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu  
305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile  
325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser  
340 345

<210> 187

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

<400> 187

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aagttttagt cttgtccacc cagaacaggc gggtattttc atg ccc acc ctc gcg 115  
Met Pro Thr Leu Ala  
1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163  
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala	
250 255 260	

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
           265                                  270                                  275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
           280                                  285                                  290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
           295                                  300                                  305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310                                  315                                  320                                  325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
                                   330                                  335                                  340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
                                   345                                  350                                  355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc  
 1219  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile  
                                   360                                  365                                  370

gag ttc tac atc taataggtat ttacgacaaa tag  
 1254  
 Glu Phe Tyr Ile  
           375

<210> 188

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
                                   20                                  25                                  30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
           35                                  40                                  45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
           50                                  55                                  60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
           65                                  70                                  75                                  80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr

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<210> 189
<211> 1210
<212> DNA
<213> Corynebacterium glutamicum
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1210)

&lt;223&gt; FRXA00403

&lt;400&gt; 189

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aagtttttagt cttgtccacc cagaacaggc gggtatttttc atg ccc acc ctc gcg 115
                                     Met Pro Thr Leu Ala
                                     1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
                10                15                20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
                25                30                35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
                40                45                50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
                55                60                65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
                70                75                80                85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
                90                95                100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
                105                110                115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
                120                125                130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
                135                140                145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
                150                155                160                165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                170                175                180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
                185                190                195

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tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739  
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg  
 200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787  
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg  
 215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835  
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg  
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883  
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat  
 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac  
 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac  
 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac  
 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg  
 1210  
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser  
 360 365 370

<210> 190

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45  
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60  
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80  
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95  
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110  
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125  
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140  
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160  
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365

Pro Ser  
 370

<210> 191  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(664)  
 <223> RXS03158

<400> 191  
 caaagctcac cgaaggcacc aacgccaaagt tgggtgttga caacaccttg gcatcccccatt 60  
 acctgcagca gccactaaaa ctccggcgccac acgcaagtcc ttg cac tcc acc acc 115  
 Leu His Ser Thr Thr  
 1 5  
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163  
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr  
 10 15 20  
 aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211  
 Asn Asp Gln Glu Met Asp Glu Glu Leu Phe Met Gln Gly Gly Ile  
 25 30 35  
 gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259  
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu  
 40 45 50  
 aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307  
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys  
 55 60 65  
 atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355  
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr  
 70 75 80 85

cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403  
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met  
 90 95 100  
 aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451  
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu  
 105 110 115  
 gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499  
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu  
 120 125 130  
 tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547  
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr  
 135 140 145  
 cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595

His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val  
 150 155 160 165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643  
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val  
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gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687  
 Glu Gln Ala Leu Asn Asn Leu  
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<210> 192  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 192  
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 35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys  
 50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val  
 65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val  
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe  
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu  
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His  
 130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val  
 145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp  
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Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu  
 180 185

<210> 193  
 <211> 617  
 <212> DNA  
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<220>

&lt;221&gt; CDS

&lt;222&gt; (1)..(594)

&lt;223&gt; FRXA00254

&lt;400&gt; 193

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Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
  1                      5                      10                      15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac      96
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
                20                      25                      30

gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga      144
Asp Gln Glu Met Asp Glu Glu Leu Phe Met Gln Gly Gly Ile Gly
          35                      40                      45

ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag      192
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
          50                      55                      60

acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc      240
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
  65                      70                      75                      80

gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca      288
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
                85                      90                      95

ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag      336
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
          100                      105                      110

cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca      384
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
          115                      120                      125

gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc      432
Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
          130                      135                      140

ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac      480
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
          145                      150                      155                      160

cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc      528
Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
          165                      170                      175

atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag      576
Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
          180                      185                      190

cag gcc ctc aat aac ctt tagaaactat ttggcgcaa gca      617
Gln Ala Leu Asn Asn Leu
          195

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&lt;210&gt; 194

&lt;211&gt; 198

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 194

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Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
 1             5             10             15

Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
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Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
      35             40             45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
      50             55             60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
      65             70             75             80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
      85             90             95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
      100            105            110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
      115            120            125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
      130            135            140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
      145            150            155            160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
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Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
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Gln Ala Leu Asn Asn Leu
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<210> 195

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA02532

<400> 195

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tgtgcaagcg ggacggccag ccagaactcc tgggtgcgccg atg aac cca cct atc    115
                               Met Asn Pro Pro Ile
                               1             5

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc    163

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Thr	Leu	Ser	Ser	Thr	Tyr	Val	His	Asp	Ser	Glu	Lys	Ala	Tyr	Gly	Arg		
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gat	ggc	aat	gat	gga	tgg	ggt	gca	ttt	gag	gct	gcc	atg	gga	act	cta	211	
Asp	Gly	Asn	Asp	Gly	Trp	Gly	Ala	Phe	Glu	Ala	Ala	Met	Gly	Thr	Leu		
		25						30					35				
gat	ggt	ggg	ttc	gcg	gta	tct	tat	tct	tca	ggt	ttg	gca	gcg	gca	acg	259	
Asp	Gly	Gly	Phe	Ala	Val	Ser	Tyr	Ser	Ser	Gly	Leu	Ala	Ala	Ala	Thr		
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tcg	att	gct	gat	ttg	gtt	cct	act	ggt	ggc	aca	gtt	gtt	tta	cct	aaa	307	
Ser	Ile	Ala	Asp	Leu	Val	Pro	Thr	Gly	Gly	Thr	Val	Val	Leu	Pro	Lys		
	55					60					65						
gct	gcc	tat	tat	ggc	gtg	acc	aat	att	ttc	gcc	agg	atg	gaa	gcc	cgc	355	
Ala	Ala	Tyr	Tyr	Gly	Val	Thr	Asn	Ile	Phe	Ala	Arg	Met	Glu	Ala	Arg		
	70				75					80					85		
gga	agg	ctg	aag	gtt	cga	act	gtt	gat	gca	gac	aat	acc	gaa	gaa	gtg	403	
Gly	Arg	Leu	Lys	Val	Arg	Thr	Val	Asp	Ala	Asp	Asn	Thr	Glu	Glu	Val		
			90						95				100				
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Ile	Ala	Ala	Ala	Gln	Gly	Ala	Asp	Val	Val	Trp	Val	Glu	Ser	Ile	Ala		
			105					110					115				
aat	ccg	acg	atg	gtg	gta	gct	gat	atc	cct	gca	ata	gtc	gac	ggt	gtg	499	
Asn	Pro	Thr	Met	Val	Val	Ala	Asp	Ile	Pro	Ala	Ile	Val	Asp	Gly	Val		
		120					125					130					
cgt	ggg	ctt	gga	gtt	ttg	act	gtc	gtt	gac	gcg	act	ttc	gca	acg	cca	547	
Arg	Gly	Leu	Gly	Val	Leu	Thr	Val	Val	Asp	Ala	Thr	Phe	Ala	Thr	Pro		
	135					140					145						
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Leu	Arg	Gln	Arg	Pro	Leu	Glu	Leu	Gly	Ala	Asp	Ile	Val	Leu	Tyr	Ser		
	150				155					160					165		
gca	acc	aaa	ctt	atc	ggt	gga	cac	tct	gat	ctt	ctt	ctt	gga	gtc	gca	643	
Ala	Thr	Lys	Leu	Ile	Gly	Gly	His	Ser	Asp	Leu	Leu	Leu	Gly	Val	Ala		
			170						175					180			
gtg	tgc	aag	tct	gag	cac	cat	gcg	cag	ttt	ctt	gcc	act	cac	cgt	cat	691	
Val	Cys	Lys	Ser	Glu	His	His	Ala	Gln	Phe	Leu	Ala	Thr	His	Arg	His		
			185					190					195				
gat	cat	ggt	tca	gtg	ccg	gga	ggt	ctt	gaa	gcg	ttt	ctt	gct	ctc	cgt	739	
Asp	His	Gly	Ser	Val	Pro	Gly	Gly	Leu	Glu	Ala	Phe	Leu	Ala	Leu	Arg		
		200					205					210					
gga	ttg	tat	tcc	ttg	gcg	gtg	cgt	ctt	gat	cga	gca	gaa	tcc	aac	gca	787	
Gly	Leu	Tyr	Ser	Leu	Ala	Val	Arg	Leu	Asp	Arg	Ala	Glu	Ser	Asn	Ala		
	215					220					225						
gca	gaa	ctt	tcg	cgg	cga	ctt	aac	gcg	cat	cct	tcg	gtt	acc	cgc	gtc	835	
Ala	Glu	Leu	Ser	Arg	Arg	Leu	Asn	Ala	His	Pro	Ser	Val	Thr	Arg	Val		
	230				235					240					245		
aat	tat	cca	gga	ctt	cct	gat	gat	ccc	caa	cat	gaa	aaa	gcc	gtg	cga	883	
Asn	Tyr	Pro	Gly	Leu	Pro	Asp	Asp	Pro	Gln	His	Glu	Lys	Ala	Val	Arg		

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Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala  
 130 135 140

Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp  
 145 150 155 160

Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu  
 165 170 175

Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu  
 180 185 190

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala  
 195 200 205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg  
 210 215 220

Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro  
 225 230 235 240

Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His  
 245 250 255

Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser  
 260 265 270

Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser  
 275 280 285

Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala  
 290 295 300

Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro  
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Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu  
 325 330 335

Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly  
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 <222> (101)..(838)  
 <223> RXS03159

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 Leu Ser Phe Asp Pro  
 1 5  
 aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163

Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro  
                   10                  15                  20

gac gac tac tac ggt tgc att aac acc cca atc tat gcc tcc acc acc 211  
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr  
                   25                  30                  35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259  
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr  
                   40                  45                  50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307  
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala  
                   55                  60                  65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355  
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala  
                   70                  75                  80                  85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403  
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val  
                   90                  95                  100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451  
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val  
                   105                  110                  115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499  
 Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val  
                   120                  125                  130

gaa gag gtc aag gca gcg atc aag gac aac acc aag ctg atc tgg gtg 547  
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val  
                   135                  140                  145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595  
 Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val  
                   150                  155                  160                  165

gca aag ctc acc gaa ggc acc aac gcc aag ttg gtt gtt gac aac acc 643  
 Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr  
                   170                  175                  180

ttg gca tcc cca tac ctg cag cag cca cta aaa ctc ggc gca cac gca 691  
 Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala  
                   185                  190                  195

agt cct tgc act cca cca cca agt aca tgc aag gac act ccg acg ttg 739  
 Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu  
                   200                  205                  210

ttg gcg gcc ttg tgg gta cca acg acc agg aaa tgg acg aag aac tgc 787  
 Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys  
                   215                  220                  225

tgt tca tgc agg gcg gca tgc gac cga tcc cat cag ttt tgc atg cat 835  
 Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His  
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acc tgaccgcccg tggcctcaag acc 861  
 Thr

<210> 198  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 198

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Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
          35              40              45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
          50              55              60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65              70              75              80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
          85              90              95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
          100              105              110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
          115              120              125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
          130              135              140

Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr
          145              150              155              160

Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu
          165              170              175

Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys
          180              185              190

Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys
          195              200              205

Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys
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Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His
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Gln Phe Ser Met His Thr
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; FRXA02768

&lt;400&gt; 199

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				Leu	Ser	Phe	Asp	Pro	
				1				5	

aac	acc	cag	ggt	ttc	tcc	act	gca	tcg	att	cac	gct	ggg	tat	gag	cca	163
Asn	Thr	Gln	Gly	Phe	Ser	Thr	Ala	Ser	Ile	His	Ala	Gly	Tyr	Glu	Pro	
			10						15					20		

gac	gac	tac	tac	ggt	tcg	att	aac	acc	cca	atc	tat	gcc	tcc	acc	acc	211
Asp	Asp	Tyr	Tyr	Gly	Ser	Ile	Asn	Thr	Pro	Ile	Tyr	Ala	Ser	Thr	Thr	
			25					30					35			

ttc	gcg	cag	aac	gct	cca	aac	gaa	ctg	cgc	aaa	ggc	tac	gag	tac	acc	259
Phe	Ala	Gln	Asn	Ala	Pro	Asn	Glu	Leu	Arg	Lys	Gly	Tyr	Glu	Tyr	Thr	
		40				45					50					

cgt	gtg	ggc	aac	ccc	acc	atc	gtg	gca	tta	gag	cag	acc	gtc	gca	gca	307
Arg	Val	Gly	Asn	Pro	Thr	Ile	Val	Ala	Leu	Glu	Gln	Thr	Val	Ala	Ala	
	55					60				65						

ctc	gaa	ggc	gca	aag	tat	ggc	cgc	gca	ttc	tcc	tcc	ggc	atg	gct	gca	355
Leu	Glu	Gly	Ala	Lys	Tyr	Gly	Arg	Ala	Phe	Ser	Ser	Gly	Met	Ala	Ala	
	70				75				80					85		

acc	gac	atc	ctg	ttc	cgc	atc	atc	ctc	aag	ccg	ggc	gat	cac	atc	gtc	403
Thr	Asp	Ile	Leu	Phe	Arg	Ile	Ile	Leu	Lys	Pro	Gly	Asp	His	Ile	Val	
			90					95					100			

ctc	ggc	aac	gat	gct	tac	ggc	gga	acc	tac	cgc	ctg	atc	gac	acc	gta	451
Leu	Gly	Asn	Asp	Ala	Tyr	Gly	Gly	Thr	Tyr	Arg	Leu	Ile	Asp	Thr	Val	
		105					110					115				

ttc	acc	gca	tgg	ggc	gtc	gaa	tac	acc	gtt	gtt	gat	acc	tcc	gtc	gtg	499
Phe	Thr	Ala	Trp	Gly	Val	Glu	Tyr	Thr	Val	Val	Asp	Thr	Ser	Val	Val	
		120				125					130					

gaa	gag	gtc	aag	gca	gcg	atc	aag	gac	aac	acc	aag	gct	gat	ctt	ggt	547
Glu	Glu	Val	Lys	Ala	Ala	Ile	Lys	Asp	Asn	Thr	Lys	Ala	Asp	Leu	Gly	
	135				140					145						

gga	aac	ccc	aac	caa	ccc	agc	act	ttg	gca	tta	ccc	gac	atc	gaa	gca	595
Gly	Asn	Pro	Asn	Gln	Pro	Ser	Thr	Leu	Ala	Leu	Pro	Asp	Ile	Glu	Ala	
	150				155				160					165		

gtn	tgc	aaa	act	tca	ccc	gaa	agg	cac	caa	ccc	caa	gct	tgt	tgt	ttg	643
Val	Cys	Lys	Thr	Ser	Pro	Glu	Arg	His	Gln	Pro	Gln	Ala	Cys	Cys	Leu	
			170					175					180			

aca	aca	cct	tcg	cat	tcc	cca	tac	ctg	cag	can	cca	ctt	aaa	ant	tnn	691
Thr	Thr	Pro	Ser	His	Ser	Pro	Tyr	Leu	Gln	Xaa	Pro	Leu	Lys	Xaa	Xaa	
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Xaa His Thr Gln  
200

703

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<213> Corynebacterium glutamicum

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Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys  
35 40 45  
Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu  
50 55 60  
Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser  
65 70 75 80  
Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro  
85 90 95  
Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg  
100 105 110  
Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val  
115 120 125  
Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr  
130 135 140  
Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu  
145 150 155 160  
~~Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro~~  
165 170 175  
Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa  
180 185 190  
Pro Leu Lys Xaa Xaa Xaa His Thr Gln  
195 200

<210> 201  
<211> 1113  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1090)  
<223> RXA00216

&lt;400&gt; 201

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ttggatcagg caccatctgc cacacggagt ctttaagaaaa ttg ggc gct tat ggt 115  
 Leu Gly Ala Tyr Gly  
 1 5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163  
 Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile  
 10 15 20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211  
 Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg  
 25 30 35

ggg ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259  
 Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met  
 40 45 50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc 307  
 Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro  
 55 60 65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat 355  
 Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp  
 70 75 80 85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa 403  
 Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln  
 90 95 100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc 451  
 Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly  
 105 110 115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg 499  
 His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala  
 120 125 130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt 547  
 Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe  
 135 140 145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt 595  
 Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu  
 150 155 160 165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643  
 Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala  
 170 175 180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691  
 Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser  
 185 190 195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739  
 Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp  
 200 205 210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat 787

Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp  
 215 220 225  
 caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc 835  
 Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr  
 230 235 240 245  
 agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883  
 Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val  
 250 255 260  
 gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc 931  
 Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg  
 265 270 275  
 ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979  
 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val  
 280 285 290  
 gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc  
 1027  
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala  
 295 300 305  
 gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag  
 1075  
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys  
 310 315 320 325  
 gat tca tgc gac ctt taaggcttta ccggcgctgg gtg  
 1113  
 Asp Ser Cys Asp Leu  
 330

<210> 202  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 202  
 Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu

1	5	10	15
Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro	20	25	30
Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val	35	40	45
Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val	50	55	60
Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu	65	70	75
Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp	85	90	95
Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile	100	105	110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg  
 115 120 125  
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys  
 130 135 140  
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro  
 145 150 155 160  
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe  
 165 170 175  
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln  
 180 185 190  
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly  
 195 200 205  
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val  
 210 215 220  
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe  
 225 230 235 240  
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr  
 245 250 255  
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala  
 260 265 270  
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr  
 275 280 285  
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly  
 290 295 300  
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser  
 305 310 315 320  
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu  
 325 330

&lt;210&gt; 203

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(600)

&lt;223&gt; RXN00402

&lt;400&gt; 203

act gac gaa aag gat gga aag cca gta ttg ccc tac ttc gtc act cca 48  
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro  
 1 5 10 15

gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96  
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala

20	25	30	
ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc			144
Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr			
35	40	45	
ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt			192
Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu			
50	55	60	
tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa			240
Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu			
65	70	75	80
ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg			288
Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu			
85	90	95	
aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac			336
Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr			
100	105	110	
acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct			384
Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala			
115	120	125	
tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc			432
Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile			
130	135	140	
ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca			480
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser			
145	150	155	160
cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc			528
Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr			
165	170	175	
gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac			576
Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp			
180	185	190	

ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca	623
Leu Glu Gly Gly Phe Ala Ala Ile	
195	200

&lt;210&gt; 204

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 204

Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
1 5 10 15

Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
20 25 30

Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
35 40 45

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
50 55 60

Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
65 70 75 80

Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu  
85 90 95

Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr  
100 105 110

Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala  
115 120 125

Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile  
130 135 140

Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser  
145 150 155 160

Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr  
165 170 175

Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp  
180 185 190

Leu Glu Gly Gly Phe Ala Ala Ile  
195 200

<210> 205

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00402

<400> 205

gta ttg ccc tac ttc gtc act cca gat gct gct tac cac gga ttg aag 48  
Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys  
1 5 10 15

tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96  
Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly  
20 25 30

ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144  
Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala  
35 40 45

gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192  
Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn  
50 55 60

gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240  
Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val

65	70	75	80	
gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc				288
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95	
aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag				336
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110	
atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag				384
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys	115	120	125	
cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt				432
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val	130	135	140	
cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca				480
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala	145	150	155	160
cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag				528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu	165	170	175	
acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc				576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile	180	185	190	
tagcttttaa tagactcacc cca				599
<210> 206				
<211> 192				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 206				
Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys				
1 5 10 15				

Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly	20	25	30
Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala	35	40	45
Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn	50	55	60
Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val	65	70	75
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys			

115	120	125
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val		
130	135	140
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala		
145	150	155
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu		
165	170	175
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile		
180	185	190

<210> 207  
 <211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> RXA00405

<400> 207  
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ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac	115
Met Pro Lys Tyr Asp	
1 5	
aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca	163
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala	
10 15 20	
ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac	211
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr	
25 30 35	
caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt	259
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg	
40 45 50	
ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca	307
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro	
55 60 65	
acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc	355
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val	
70 75 80 85	
cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att	403
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile	
90 95 100	
ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc	451
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu	

105	110	115	
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt			499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly			
120	125	130	
atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag			547
Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln			
135	140	145	
gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc			595
Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala			
150	155	160	165
aac cca cag gca gac gtc			613
Asn Pro Gln Ala Asp Val			
170			

&lt;210&gt; 208

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 208

Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr			
1	5	10	15
Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg			
20	25	30	
Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu			
35	40	45	
His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser			
50	55	60	
Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser			
65	70	75	80
Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala			
85	90	95	

Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val		
100	105	110

Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr		
115	120	125

Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp		
130	135	140

Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe		
145	150	155

Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val	
165	170

&lt;210&gt; 209

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(528)

&lt;223&gt; RXA02197

&lt;400&gt; 209

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gcc gaa cgc atg cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc      48
Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
   1                               10                               15

ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac      96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
                20                25                30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct      144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
                35                40                45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag      192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
                50                55                60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc      240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
   65                70                75                80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt      288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
                85                90                95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac      336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
                100                105                110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct      384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
                115                120                125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt      432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
                130                135                140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc      480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
                145                150                155                160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc      528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
                165                170                175

taacaccttt gagaggaaa act      551

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&lt;210&gt; 210

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 210

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe  
 1 5 10 15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175

&lt;210&gt; 211

&lt;211&gt; 2599

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2599)

&lt;223&gt; RXN02198

&lt;400&gt; 211

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agttcgggaa ttgtctaata cgtactaagc tgtctacaca atg tct act tca gtt 115  
 Met Ser Thr Ser Val  
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu

25	30	35	
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly 40 45 50			259
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile 55 60 65			307
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr 70 75 80 85			355
ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg 90 95 100			403
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala 105 110 115			451
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly 120 125 130			499
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr 135 140 145			547
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp 150 155 160 165			595
ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln 170 175 180			643
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 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu  
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Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys  
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1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
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1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
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1699

Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
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Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
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Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
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Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
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Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
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2035

Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
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2131

Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
665 670 675

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2179

Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
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Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
695 700 705

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2323

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Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
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2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

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2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
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Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
790 795 800 805

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2563

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<213> Corynebacterium glutamicum

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Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
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Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
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Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
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Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
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Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
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Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
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Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
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Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
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Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
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Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
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Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
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Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
 245 250 255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
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Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
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Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
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Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
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Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
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 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
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 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
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 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
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 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
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 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys

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Ala	Gln	Arg	Ile	Ile	Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu							
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Glu	Ala	Gly	Met	Lys	Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp							
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Leu	Leu	Asn	Gly	Met	Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln							
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Val	Ala	Tyr	Leu	Glu	Pro	Phe	Met	Glu	Glu	Glu	Ala	Glu	Ala	Thr	Gly							
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Ser	Ala	Gln	Ala	Glu	Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys							
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Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser							
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 Met Ser Thr Ser Val  
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 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
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Leu	Ala	Asn	His	Val	Leu	Ile	Gly	Asp	Gly	Ala	Met	Gly	Thr	Gln	Leu	
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caa	ggc	ttt	gac	ctg	gac	gtg	gaa	aag	gat	ttc	ctt	gat	ctg	gag	ggg	259
Gln	Gly	Phe	Asp	Leu	Asp	Val	Glu	Lys	Asp	Phe	Leu	Asp	Leu	Glu	Gly	
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Cys	Asn	Glu	Ile	Leu	Asn	Asp	Thr	Arg	Pro	Asp	Val	Leu	Arg	Gln	Ile	
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His	Arg	Ala	Tyr	Phe	Glu	Ala	Gly	Ala	Asp	Leu	Val	Glu	Thr	Asn	Thr	
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ttt	ggg	tgc	aac	ctg	ccg	aac	ttg	gcg	gat	tat	gac	atc	gct	gat	cgt	403
Phe	Gly	Cys	Asn	Leu	Pro	Asn	Leu	Ala	Asp	Tyr	Asp	Ile	Ala	Asp	Arg	
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Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala	
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Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly	
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Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr	
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gca	gat	ttg	cgt	ggg	cac	tac	aag	gaa	gca	gcg	ctt	ggc	atc	atc	gac	595
Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp	
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Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp	
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Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr	
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1747

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1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
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1987

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2035

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2083

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2131

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665 670 675

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2179

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680 685 690

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2227

Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
2275

Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
2323

Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
2371

Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
2419

Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac  
2467

Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca  
2515

Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg  
2563

Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
810 815 820

aag tcc acc gtg gtg  
2578

Lys Ser Thr Val Val  
825

<210> 214

<211> 826

<212> PRT

<213> Corynebacterium glutamicum

&lt;400&gt; 214

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser  
1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala  
20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
85 90 95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
130 135 140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
165 170 175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
180 185 190

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
195 200 205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
210 215 220

Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
225 230 235 240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
245 250 255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
260 265 270

Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
275 280 285

Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
290 295 300

Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
305 310 315 320

Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
 340 345 350  
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
 355 360 365  
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
 370 375 380  
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln  
 385 390 395 400  
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala  
 500 505 510  
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys  
 515 520 525  
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu  
 530 535 540  
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu  
 545 550 555 560  
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile  
 565 570 575  
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe  
 580 585 590  
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser  
 595 600 605  
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val  
 610 615 620  
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu  
 625 630 635 640  
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys

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<210> 215
<211> 621
<212> DNA
<213> Corynebacterium glutamicum
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 $\langle 220 \rangle$ 

~~221 GDC~~

<222> (101) . . (598)

<223> RXN03074

<400> 215

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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
Met Thr Gln Ser Ala  
1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
           40                          45                          50  
  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
           55                          60                          65  
  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
           70                          75                          80                          85  
  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                           90                          95                          100  
  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                           105                          110                          115  
  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
                           120                          125                          130  
  
 gac gta gtg gta tgc att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
  
 cag taatttgttt tgacgacgca gta 621  
 Gln

&lt;210&gt; 216

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
   1                          5                          10                          15  
  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                           85                          90                          95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160

Glu Ala Pro Ile Lys Gln  
 165

&lt;210&gt; 217

&lt;211&gt; 621

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(598)

&lt;223&gt; FRXA02906

&lt;400&gt; 217

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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
 Met Thr Gln Ser Ala  
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130  
  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
  
 cag taatttggtt tgacgacgca gta 621  
 Gln

<210> 218  
 <211> 166  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 218  
 Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
       1                          5                          10                          15  
  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
           85                          90                          95  
  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
           100                          105                          110  
  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
           115                          120                          125  
  
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
           130                          135                          140  
  
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
           145                          150                          155                          160  
  
 Glu Ala Pro Ile Lys Gln  
                           165

<210> 219  
 <211> 1557  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1534)

&lt;223&gt; RXN00132

&lt;400&gt; 219

aacagcttca atcaattcgg tgtccactcc aacatgtaga gtggtgcgcg ttaaaaaagt 60

tttcctaatt ttcattttct taaaaggagc tgcgcaggac atg gca cag gtt atg 115  
 Met Ala Gln Val Met  
 1 5

gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163  
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln  
 10 15 20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211  
 Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys  
 25 30 35

gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct 259  
 Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser  
 40 45 50

atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct 307  
 Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala  
 55 60 65

ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag 355  
 Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln  
 70 75 80 85

gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag 403  
 Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu  
 90 95 100

cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag 451  
 Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu  
 105 110 115

tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca 499  
 Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro  
 120 125 130

aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc 547  
 Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg  
 135 140 145

ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac 595  
 Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn  
 150 155 160 165

gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt 643  
 Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu  
 170 175 180

gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt 691  
 Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly  
 185 190 195

gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct 739  
 Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala  
 200 205 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc 787  
 Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val  
 215 220 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc 835  
 Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile  
 230 235 240 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg 883  
 Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val  
 250 255 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931  
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe  
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979  
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn  
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag  
 1027  
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu  
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac  
 1075  
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp  
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg  
 1123  
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu  
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg  
 1171  
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu  
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag  
 1219  
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu  
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc  
 1267  
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc  
 1315  
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser  
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac  
 1363

Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn  
410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac  
1411

Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp  
425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc  
1459

Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr  
440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc  
1507

Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly  
455 460 465

cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag  
1554

Pro Phe Lys Pro Glu His Tyr Arg Tyr  
470 475

gga  
1557

<210> 220

<211> 478

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu  
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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu  
20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly Ser  
85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro

145                      150                      155                      160  
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met  
                                  165                                   170                                   175  
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala  
                                  180                                   185                                   190  
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg  
                                  195                                   200                                   205  
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn  
                                  210                                   215                                   220  
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr  
                                  225                                   230                                   235                                   240  
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met  
                                  245                                   250                                   255  
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly  
                                  260                                   265                                   270  
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu  
                                  275                                   280                                   285  
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val  
                                  290                                   295                                   300  
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala  
                                  305                                   310                                   315                                   320  
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys  
                                  325                                   330                                   335  
 Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp  
                                  340                                   345                                   350  
 Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys  
                                  355                                   360                                   365  
 Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val  
                                  370                                   375                                   380  
 Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro  
                                  385                                   390                                   395                                   400  
 Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile  
                                  405                                   410                                   415  
 Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu  
                                  420                                   425                                   430  
 Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu  
                                  435                                   440                                   445  
 Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly  
                                  450                                   455                                   460  
 Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr  
                                  465                                   470                                   475

<210> 221  
 <211> 128  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(105)  
 <223> FRXA00132

<400> 221  
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 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln  
       1                  5                  10                  15  
  
 gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
                   20                  25                  30  
  
 tac cgc tac taatgattgt cagcattgag gga 128  
 Tyr Arg Tyr  
           35

<210> 222  
 <211> 35  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 222  
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln  
       1                  5                  10                  15  
  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
                   20                  25                  30  
  
 Tyr Arg Tyr  
           35

<210> 223  
 <211> 1396  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1396)  
 <223> FRXA01371

<400> 223  
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   Met Ala Gln Val Met  
   1                  5  
  
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163  
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln

	10	15	20	
att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag				211
Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys				
	25	30	35	
gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct				259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser				
	40	45	50	
atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct				307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala				
	55	60	65	
ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag				355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln				
	70	75	80	85
gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag				403
Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu				
	90	95	100	
cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag				451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu				
	105	110	115	
tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca				499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro				
	120	125	130	
aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc				547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg				
	135	140	145	
ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac				595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn				
	150	155	160	165
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt				643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu				
	170	175	180	
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt				691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly				
	185	190	195	
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct				739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala				
	200	205	210	
gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc				787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val				
	215	220	225	
acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc				835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile				
	230	235	240	245
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg				883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val				
	250	255	260	



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 Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu  
 20 25 30  
 Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
 35 40 45  
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
 50 55 60  
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
 65 70 75 80  
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly Ser  
 85 90 95  
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
 100 105 110  
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
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 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
 130 135 140  
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro  
 145 150 155 160  
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met  
 165 170 175  
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala  
 180 185 190  
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg  
 195 200 205  
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn  
 210 215 220  
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr  
 225 230 235 240  
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met  
 245 250 255  
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly  
 260 265 270  
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu  
 275 280 285  
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val  
 290 295 300  
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala  
 305 310 315 320  
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys

	325		330		335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp	340		345		350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys	355		360		365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val	370		375		380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro	385		390		395
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile	405		410		415
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 Met Thr Ser Asn Phe  
 1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163  
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Gly Leu  
 10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211  
 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu  
 25 30 35

ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259  
 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu  
 40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307  
 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala  
 55 60 65

atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355  
 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp  
 70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403  
 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg  
 90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451  
 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met  
 105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499  
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser  
 120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547  
 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu  
 135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595  
 Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly  
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cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643  
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 170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691  
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys  
 185 190 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739  
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787  
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr  
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 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883  
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
1123

Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
1171

Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
1219

Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
1267

Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
1315

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
1363

Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
1411

Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
1459

Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
455 460 465

ggg gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
550 555 560 565

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1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga  
1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg  
585 590 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc  
1939

Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg  
600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg  
1987

Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met  
615 620 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat  
2035

Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp  
630 635 640 645

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2083

Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu  
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg  
2131

Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val  
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt  
2179

Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc  
2227

Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct  
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc  
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
730 735 740

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2358

Gly Ala Thr Ile  
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<210> 226

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

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Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
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Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
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 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala  
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
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 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
 420 425 430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
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 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
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<212> DNA

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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu				
	40	45	50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca				307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala				
	55	60	65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat				355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp				
	70	75	80	85
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc				403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg				
	90	95	100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg				451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met				
	105	110	115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct				499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser				
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gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc				547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu				
	135	140	145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt				595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly				
	150	155	160	165
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct				643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro				
	170	175	180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag				691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys				
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tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc				739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr				
	200	205	210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act				787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr				
	215	220	225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc				835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly				
	230	235	240	245
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc				883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly				
	250	255	260	

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
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 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
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 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
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 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

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 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
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 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

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 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

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 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
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 425 430 435

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 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
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 1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
 1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
 1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
 570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg  
 1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr  
 585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt  
 1923

Arg Arg Arg  
 600

<210> 228

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly  
 1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser  
 20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
 35 40 45  
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
 50 55 60  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 65 70 75 80  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
 85 90 95  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
 100 105 110  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
 115 120 125  
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
 130 135 140  
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
 145 150 155 160  
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
 165 170 175  
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
 180 185 190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
 195 200 205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala

355                      360                      365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
     370                      375                      380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385                      390                      395                      400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
                     405                      410                      415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
                     420                      425                      430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
                     435                      440                      445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
                     450                      455                      460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465                      470                      475                      480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
                     485                      490                      495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
                     500                      505                      510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
                     515                      520                      525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr  
                     530                      535                      540  
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr  
 545                      550                      555                      560  
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
                     565                      570                      575  
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
                     580                      585                      590  
 Leu Leu Pro Ala Thr Arg Arg Arg  
                     595                      600

&lt;210&gt; 229

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; FRXA02086

&lt;400&gt; 229

gatgatcagc cgctggctac cactgctgac caggttgac tggcactgcg cgatgaaatt 60

aac 603

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<400> 230
Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
  1             5             10             15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
      20             25             30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35             40             45

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Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60  
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95  
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110  
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
 115 120 125  
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
 130 135 140  
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 145 150 155 160

<210> 231  
 <211> 1326  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1303)  
 <223> RXN02648

<400> 231  
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 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5  
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50  
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg

70	75	80	85	
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa				403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu				
	90	95	100	
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat				451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp				
	105	110	115	
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct				499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser				
	120	125	130	
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga				547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly				
	135	140	145	
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg				595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu				
	150	155	160	165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca				643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala				
	170	175	180	
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac				691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp				
	185	190	195	
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa				739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu				
	200	205	210	
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg				787
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro				
	215	220	225	
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag				835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys				
	230	235	240	245
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac aat gca				883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala				
	250	255	260	
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc				931
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly				
	265	270	275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att				979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile				
	280	285	290	
ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca				
1027				
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala				
	295	300	305	
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt				
1075				

Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
 1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
 1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
 1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
 1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
 1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 390 395 400

aacgagggtt gct  
 1326

<210> 232

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
210 215 220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
225 230 235 240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
245 250 255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
260 265 270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
275 280 285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
290 295 300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
305 310 315 320

Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
385 390 395 400

Phe

<210> 233

<211> 548

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(525)

&lt;223&gt; FRXA02648

&lt;400&gt; 233

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gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca      48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1                      5                      10                      15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc      96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20                      25                      30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc      144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35                      40                      45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt      192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
          50                      55                      60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc      240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
          65                      70                      75                      80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa      288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
          85                      90                      95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac      336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
          100                      105                      110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt      384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
          115                      120                      125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac      432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
          130                      135                      140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg      480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
          145                      150                      155                      160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc      525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          165                      170                      175

taagctagac aacgagggtt gct      548

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&lt;210&gt; 234

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 234

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1                      5                      10                      15

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Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

&lt;210&gt; 235

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(784)

&lt;223&gt; FRXA02658

&lt;400&gt; 235

atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcggttag agtcgaatga 60

gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85  
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu  
 90 95 100  
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
 105 110 115  
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
 120 125 130  
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
 135 140 145  
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
 150 155 160 165  
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643  
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
 170 175 180  
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
 185 190 195  
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210  
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784  
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

&lt;210&gt; 236

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 236

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu